

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 9, 2004, 10:53:58 ; Search time 53.0897 Seconds  
(without alignments)  
654.615 Million cell updates/sec

Title: US-09-880-748-2\_COPY\_1\_123  
Perfect score: 640  
Sequence: 1 QVQLQSGAEVKKKFGSSVRV.....LFPHYGMDVGRGTMTVSS 123

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues  
1 number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 70 summaries

Database : A\_Geneseq\_29Jan04:.\*  
1: geneseqp1980s:.\*  
2: geneseqp1990s:.\*  
3: geneseqp2000s:.\*  
4: geneseqp2001s:.\*  
5: geneseqp2002s:.\*  
6: geneseqp2003as:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	640	100.0	246	5	ABP44917 Human Bly
2	640	100.0	249	5	ABP44468 Human Bly
3	640	100.0	249	5	ABP43991 Human Bly
4	640	100.0	249	5	ABP44708 Human Bly
5	640	100.0	249	5	ABP44460 Human Bly
6	640	100.0	249	5	ABP44785 Human Bly
7	640	100.0	249	5	ABP44607 Human Bly
8	637	99.5	246	5	ABP45415 Human Bly
9	637	99.5	246	5	ABP45770 Human Bly
10	637	99.5	249	5	ABP44602 Human Bly
11	634	99.1	249	5	ABP44688 Human Bly
12	634	99.1	249	5	ABP45737 Human Bly
13	633	98.9	246	5	ABP45297 Human Bly
14	632	98.8	249	5	ABP44677 Human Bly
15	632	98.8	249	5	ABP44313 Human Bly
16	631	98.6	246	5	ABP45807 Human Bly
17	631	98.6	249	5	ABP44710 Human Bly
18	626	97.8	249	5	ABP44775 Human Bly
19	626	97.8	249	5	ABP44783 Human Bly
20	626	97.8	249	5	ABP44793 Human Bly
21	623	97.3	249	5	ABP44314 Human Bly
22	623	97.3	249	5	ABP44750 Human Bly
23	623	97.3	249	5	ABP44804 Human Bly
24	621	97.0	249	5	ABP44450 Human Bly
25	621	97.0	249	5	ABP44800 Human Bly

## ALIGNMENTS

26	621	97.0	249	5	ABP44763	Abp44763 Human Bly
27	621	97.0	249	5	ABP44311	Abp44311 Human Bly
28	621	97.0	249	5	ABP44815	Abp44815 Human Bly
29	621	97.0	249	5	ABP44741	Abp44741 Human Bly
30	621	97.0	249	5	ABP44318	Abp44318 Human Bly
31	621	97.0	249	5	ABP44781	Abp44781 Human Bly
32	621	97.0	249	5	ABP44786	Abp44786 Human Bly
33	621	97.0	249	5	ABP44797	Abp44797 Human Bly
34	621	97.0	249	5	ABP44814	Abp44814 Human Bly
35	621	97.0	249	5	ABP44733	Abp44733 Human Bly
36	620	96.9	249	5	ABP44522	Abp44522 Human Bly
37	620	96.9	249	5	ABP44698	Abp44698 Human Bly
38	620	96.9	249	5	ABP44718	Abp44718 Human Bly
39	619	96.7	249	5	ABP44787	Abp44787 Human Bly
40	619	96.7	249	5	ABP44803	Abp44803 Human Bly
41	618	96.6	249	5	ABP44561	Abp44561 Human Bly
42	618	96.6	249	5	ABP44680	Abp44680 Human Bly
43	618	96.6	249	5	ABP44687	Abp44687 Human Bly
44	618	96.6	249	5	ABP44690	Abp44690 Human Bly
45	618	96.6	249	5	ABP44777	Abp44777 Human Bly
46	618	96.6	249	5	ABP44731	Abp44731 Human Bly
47	617	96.4	249	5	ABP44794	Abp44794 Human Bly
48	617	96.4	249	5	ABP44434	Abp44434 Human Bly
49	617	96.4	249	5	ABP44801	Abp44801 Human Bly
50	617	96.4	249	5	ABP44639	Abp44639 Human Bly
51	617	96.4	249	5	ABP44684	Abp44684 Human Bly
52	617	96.4	249	5	ABP44416	Abp44416 Human Bly
53	617	96.4	249	5	ABP44762	Abp44762 Human Bly
54	616	96.2	249	5	ABP44809	Abp44809 Human Bly
55	616	96.2	249	5	ABP44759	Abp44759 Human Bly
56	616	96.2	249	5	ABP44663	Abp44663 Human Bly
57	616	96.2	249	5	ABP44310	Abp44310 Human Bly
58	616	96.2	249	5	ABP44580	Abp44580 Human Bly
59	615	96.1	249	5	ABP44817	Abp44817 Human Bly
60	615	96.1	249	5	ABP44572	Abp44572 Human Bly
61	615	96.1	249	5	ABP44717	Abp44717 Human Bly
62	615	96.1	249	5	ABP44792	Abp44792 Human Bly
63	615	96.1	249	5	ABP44605	Abp44605 Human Bly
64	614	95.9	249	5	ABP44745	Abp44745 Human Bly
65	614	95.9	249	5	ABP44776	Abp44776 Human Bly
66	614	95.9	249	5	ABP44636	Abp44636 Human Bly
67	614	95.9	249	5	ABP44780	Abp44780 Human Bly
68	614	95.9	249	5	ABP44819	Abp44819 Human Bly
69	614	95.9	249	5	ABP44779	Abp44779 Human Bly
70	614	95.9	249	5	ABP44702	Abp44702 Human Bly

RESULT 1  
ABP44917  
ID ABP44917 standard; protein; 246 AA.  
AC ABP44917;  
DT 19-ATG-2002 (first entry)  
DE Human Blys binding scFv SEQ ID 928.  
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
OS Homo sapiens.  
PN WO200202641-A1.  
PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.  
XX  
XX 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
PI WPI; 2002-114799/15.  
XX  
XX Antibodies against B lymphocyte stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.  
XX  
XX Claim 1; Page 1509-1510; 3148pp; English.  
XX  
XX This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumor necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
XX SQ Sequence 246 AA;  
XX  
XX Query Match 100.0%; Score 640; DB 5; Length 246;  
XX Best Local Similarity 100.0%; Pred. No. 9.9e-52;  
XX Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 QVQLQSGAEVKKPGSSVRVSCKASGCTFNNAIMWVROAPQGGLMMGGIIPMGITAKY 60  
XX 1 QVQLQSGAEVKKPGSSVRVSCKASGCTFNNAIMWVROAPQGGLMMGGIIPMGITAKY 60  
XX  
XX 61 SONFGQRAVITADESTASTMELSLRSEDTAVVYCARSDLLLPHYGMDVWGRTWYT 120  
XX 61 SONFGQRAVITADESTASTMELSLRSEDTAVVYCARSDLLLPHYGMDVWGRTWYT 120  
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XX DB 121 VSS 123  
XX 121 VSS 123  
XX 121 VSS 123  
XX  
XX DB 121 VSS 123  
XX  
XX 19-AUG-2002 (first entry)  
XX  
XX Human Blys binding scFv SEQ ID 479.  
XX  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX tumor necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
XX RESULT 2  
XX ABP44468  
XX ID ABP44468 standard; protein; 249 AA.  
XX  
XX AC ABP44468;  
XX  
XX 19-AUG-2002 (first entry)  
XX  
XX Human Blys binding scFv SEQ ID 479.  
XX  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX tumor necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
XX

XX  
XX OS Homo sapiens.  
XX  
XX PN WO200202641-A1.  
XX  
XX 10-JAN-2002.  
XX  
XX 15-JUN-2001; 2001WO-US019110.  
XX  
XX 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
PI WPI; 2002-114799/15.  
XX  
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.  
XX  
XX Claim 1; Page 974-975; 3148pp; English.  
XX  
XX This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumor necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
XX SQ Sequence 249 AA;  
XX  
XX Query Match 100.0%; Score 640; DB 5; Length 249;  
XX Best Local Similarity 100.0%; Pred. No. 9.9e-52;  
XX Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 QVQLQSGAEVKKPGSSVRVSCKASGCTFNNAIMWVROAPQGGLMMGGIIPMGITAKY 60  
XX 1 QVQLQSGAEVKKPGSSVRVSCKASGCTFNNAIMWVROAPQGGLMMGGIIPMGITAKY 60  
XX  
XX 61 SONFGQRAVITADESTASTMELSLRSEDTAVVYCARSDLLLPHYGMDVWGRTWYT 120  
XX 61 SONFGQRAVITADESTASTMELSLRSEDTAVVYCARSDLLLPHYGMDVWGRTWYT 120  
XX  
XX DB 121 VSS 123  
XX 121 VSS 123  
XX 121 VSS 123  
XX  
XX DB 121 VSS 123  
XX  
XX 19-AUG-2002 (first entry)  
XX  
XX Human Blys binding scFv SEQ ID 2.  
XX  
XX RESULT 3  
XX ABP43991  
XX ID ABP43991 standard; protein; 249 AA.  
XX  
XX AC ABP43991;  
XX  
XX 19-AUG-2002 (first entry)  
XX  
XX Human Blys binding scFv SEQ ID 2.  
XX  
XX

XX Blys: B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KM common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US019110.  
XX  
PR 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
PT Antibodies against B lymphocyte stimulating polypeptides, useful for the  
XX diagnosis and treatment of cancers and immune disorders.  
XX  
PS Claim 1; Page 408-409; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 249 AA;  
XX  
Query Match 100.0%; Score 640; DB 5; Length 249;  
Best Local Similarity 100.0%; Pred. No. 9.9e-52;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVQLQDSGAEVKKPKSSVRVSCAKSGTFFNNNAIMNVRQAPQGLEMGGIIPMEGTARY 60  
DB 1 QVQLQDSGAEVKKPKSSVRVSCAKSGTFFNNNAIMNVRQAPQGLEMGGIIPMEGTARY 60  
QY 61 SONFGRAVITADESTSTASMEISLRSEDTAVVYTCARSDLLFPHYGMDVWGRTWT 120  
DB 61 SONFGRAVITADESTSTASMEISLRSEDTAVVYTCARSDLLFPHYGMDVWGRTWT 120  
QY 121 VSS 123  
DB 121 VSS 123  
RESULT 4  
ABP44708

ID ABP44708 standard; protein; 249 AA.  
XX  
AC ABP44708;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scFv SEQ ID 719.  
XX  
KM Blys: B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KM common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US019110.  
XX  
PR 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
PT Antibodies against B lymphocyte stimulating polypeptides, useful for the  
XX diagnosis and treatment of cancers and immune disorders.  
XX  
PS Claim 1; Page 1259-1260; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 249 AA;  
XX  
Query Match 100.0%; Score 640; DB 5; Length 249;  
Best Local Similarity 100.0%; Pred. No. 9.9e-52;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVQLQDSGAEVKKPKSSVRVSCAKSGTFFNNNAIMNVRQAPQGLEMGGIIPMEGTARY 60  
DB 1 QVQLQDSGAEVKKPKSSVRVSCAKSGTFFNNNAIMNVRQAPQGLEMGGIIPMEGTARY 60  
QY 61 SONFGRAVITADESTSTASMEISLRSEDTAVVYTCARSDLLFPHYGMDVWGRTWT 120  
DB 61 SONFGRAVITADESTSTASMEISLRSEDTAVVYTCARSDLLFPHYGMDVWGRTWT 120

QY 121 VSS 123  
121 VSS 123

RESULT 5  
ABP44460

ID ABP44460 standard; protein; 249 AA.

AC ABP44460;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 471.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

DR WPI; 2002-114799/15.

XX WPI; 2002-114799/15.

PT Antibodies against B lymphocyte stimulating polypeptides, useful for the

PT diagnosis and treatment of cancers and immune disorders.

XX Claim 1; Page 965-966; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to  
XX B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
XX tumour necrosis factor (TNF) super family and induces B cell  
XX proliferation and differentiation. The antibodies of the invention have  
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
XX antirheumatic and antiAIDS activity and can be used in vaccines to  
XX inhibit the expression and activity of Blys. The antibodies bind to Blys  
XX and so may be used to detect and quantitate the presence of Blys in  
XX biological samples and may be used in this way to diagnose disease  
XX associated with aberrant expression of Blys. They may also be  
XX administered to treat diseases associated with aberrant Blys expression  
XX and actively such as cancer, immune, and autoimmune disorders and  
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
XX the antibodies and fragments of the antibodies described in the method of  
XX the invention

XX Sequence 249 AA;

Query Match 100.0%; Score 640; DB 5; Length 249;

Best Local Similarity 100.0%; Pred. No. 9.9e-52;

Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 121 VSS 123  
121 VSS 123

RESULT 6  
ABP44785

ID ABP44785 standard; protein; 249 AA.

AC ABP44785;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 796.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

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PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

DR WPI; 2002-114799/15.

XX WPI; 2002-114799/15.

PT Antibodies against B lymphocyte stimulating polypeptides, useful for the

PT diagnosis and treatment of cancers and immune disorders.

XX Claim 1; Page 1351-1352; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to  
XX B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
XX tumour necrosis factor (TNF) super family and induces B cell  
XX proliferation and differentiation. The antibodies of the invention have  
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
XX antirheumatic and antiAIDS activity and can be used in vaccines to  
XX inhibit the expression and activity of Blys. The antibodies bind to Blys  
XX and so may be used to detect and quantitate the presence of Blys in  
XX biological samples and may be used in this way to diagnose disease  
XX associated with aberrant expression of Blys. They may also be  
XX administered to treat diseases associated with aberrant Blys expression  
XX and actively such as cancer, immune, and autoimmune disorders and  
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
XX the antibodies and fragments of the antibodies described in the method of  
XX the invention



OS	Homo sapiens.
XX	
PN	WO200202641-A1.
XX	
PD	10-JAN-2002.
XX	
PF	15-JUN-2001; 2001WO-US019110.
XX	
PR	16-JUN-2000; 2000US-0212210P.
PR	17-OCT-2000; 2000US-0240816P.
PR	16-MAR-2001; 2001US-0276248P.
PR	21-MAR-2001; 2001US-0277379P.
PR	25-MAY-2001; 2001US-0293499P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX	
PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX	
DR	WPI; 2002-114799/15.
XX	
PT	Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.

OS	Homo sapiens.
XX	
PN	WO200202641-A1.
XX	
PD	10-JAN-2002.
XX	
PF	15-JUN-2001; 2001WO-US019110.
XX	
PR	16-JUN-2000; 2000US-0212210P.
PR	17-OCT-2000; 2000US-0240816P.
PR	16-MAR-2001; 2001US-0276248P.
PR	21-MAR-2001; 2001US-0277379P.
PR	25-MAY-2001; 2001US-0293499P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
DA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
XX Antibodies against B lymphocyte stimulating polypeptides, useful for the  
XX diagnosis and treatment of cancers and immune disorders.  
XX  
XX Claim 1, Page 1133-1134; 3148pp; English.  
XX  
XX This invention describes novel antibodies that immunospecifically bind to  
XX B lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the  
XX tumor necrosis factor (TNF) super family and induces B cell  
XX proliferation and differentiation. The antibodies of the invention have  
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
XX antirheumatic and antiAIDS activity and can be used in vaccines to  
XX inhibit the expression and activity of BLyS. The antibodies bind to BLyS  
XX and so may be used to detect and quantitate the presence of BLyS in  
XX biological samples and may be used in this way to diagnose disease  
XX associated with aberrant expression of BLyS. They may also be  
XX administered to treat diseases associated with aberrant BLyS expression  
XX and activity such as cancer, immune, and autoimmune disorders and  
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
XX the antibodies and fragments of the antibodies described in the method of  
XX the invention  
XX  
XX Sequence 249 AA;  
XX  
XX

Query Match 99.5%; Score 637; DB 5; Length 249;  
Best Local Similarity 99.2%; Pred. No. 1,9e-51;  
Matches 122; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGAEVKKPGSSVRVSCKASGCTFNNAIMVWRQAPQGLEMGGIIPMFETAKY 60  
DB 1 QVQLQSGAEVKKPGSSVRVSCKASGCTFNNAIMVWRQAPQGLEMGGIIPMFETAKY 60  
QY 61 SONFGQRAVITADESTSTSMELSLRSEDTAVYVCARSDLLPPHYGMDVWGRTWNT 120  
DB 61 SONFGQRAVITADESTSTSMELSLRSEDTAVYVCARSDLLPPHYGMDVWGRTWNT 120  
QY 121 VSS 123  
DB 121 VSS 123

## RESULT 11

ABP44688 standard; protein; 249 AA.

ABP44688;

19-AUG-2002 (first entry)

Human BLyS binding scFv SEQ ID 699.

XX BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX tumor necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
XX Homo sapiens.  
XX OS  
XX WO200202641-A1.  
XX PN  
XX 10-JAN-2002.  
XX  
XX 15-JUN-2001; 2001WO-US019110.  
XX PF  
XX 16-JUN-2000; 2000US-0212210P.  
XX PR

PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
XX diagnosis and treatment of cancers and immune disorders.  
XX  
XX Claim 1, Page 1235-1236; 3148pp; English.  
XX  
XX

XX This invention describes novel antibodies that immunospecifically bind to  
XX B lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the  
XX tumor necrosis factor (TNF) super family and induces B cell  
XX proliferation and differentiation. The antibodies of the invention have  
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
XX antirheumatic and antiAIDS activity and can be used in vaccines to  
XX inhibit the expression and activity of BLyS. The antibodies bind to BLyS  
XX and so may be used to detect and quantitate the presence of BLyS in  
XX biological samples and may be used in this way to diagnose disease  
XX associated with aberrant expression of BLyS. They may also be  
XX administered to treat diseases associated with aberrant BLyS expression  
XX and activity such as cancer, immune, and autoimmune disorders and  
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
XX the antibodies and fragments of the antibodies described in the method of  
XX the invention  
XX  
XX Sequence 249 AA;  
XX  
XX

Query Match 99.1%; Score 634; DB 5; Length 249;  
Best Local Similarity 99.2%; Pred. No. 3.6e-51;  
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQSGAEVKKPGSSVRVSCKASGCTFNNAIMVWRQAPQGLEMGGIIPMFETAKY 60  
DB 1 QVQLQSGAEVKKPGSSVRVSCKASGCTFNNAIMVWRQAPQGLEMGGIIPMFETAKY 60  
QY 61 SONFGQRAVITADESTSTSMELSLRSEDTAVYVCARSDLLPPHYGMDVWGRTWNT 120  
DB 61 SONFGQRAVITADESTSTSMELSLRSEDTAVYVCARSDLLPPHYGMDVWGRTWNT 120  
QY 121 VSS 123  
DB 121 VSS 123

## RESULT 12

ABP45737 standard; protein; 249 AA.

ABP45737;

19-AUG-2002 (first entry)

Human BLyS binding scFv SEQ ID 1748.

XX BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX tumor necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
XX Homo sapiens.  
XX OS  
XX





XX 19-AUG-2002 (first entry)  
DT Human Blys binding scFv SEQ ID 688.  
XX  
XX  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX Homo sapiens.  
XX WO200202641-A1.  
XX  
XX 10-JAN-2002.  
XX  
XX 15-JUN-2001; 2001WO-US019110.  
XX  
XX 16-JUN-2000; 2000US-0212210P.  
XX 17-OCT-2000; 2000US-0240816P.  
XX 16-MAR-2001; 2001US-0276248P.  
XX 21-MAR-2001; 2001US-0277379P.  
XX 25-MAY-2001; 2001US-0293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
XX diagnosis and treatment of cancers and immune disorders.  
XX  
XX Claim 1, Page 1222-1223; 3148pp; English.  
XX  
XX This invention describes novel antibodies that immunospecifically bind to  
XX B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
XX tumour necrosis factor (TNF) super family and induces B cell  
XX proliferation and differentiation. The antibodies of the invention have  
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
XX antirheumatic and antiAIDS activity and can be used in vaccines to  
XX inhibit the expression and activity of Blys. The antibodies bind to Blys  
XX and so may be used to detect and quantitate the presence of Blys in  
XX biological samples and may be used in this way to diagnose disease  
XX associated with aberrant expression of Blys. They may also be  
XX administered to treat diseases associated with aberrant Blys expression  
XX and activity such as cancer, immune, and autoimmune disorders and  
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
XX the antibodies and fragments of the antibodies described in the method of  
XX the invention  
XX  
XX Sequence 249 AA;  
SQ  
Query Match 98.8%; Score 632; DB 5; Length 249;  
Best Local Similarity 99.2%; Pred. No. 5.5e-51;  
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QVQLQSGAEVKKRPGSSVRVSCAKSGCTFNNAIMNVRQAPQGLEWMGCIIPMFCTAKY 60  
DB 1 QVQLQSGAEVKKRPGSSVRVSCAKSGCTFNNAIMNVRQAPQGLEWMGCIIPMFCTAKY 60  
QY 61 SQNFGQVAITADESTASTMELSLRSEDTAVYYCARSRDLLLPFGYGDVWGRTMTY 120  
DB 61 SQNFGQVAITADESTASTMELSLRSEDTAVYYCARSRDLLLPFGYGDVWGRTMTY 120  
QY 121 VSS 123  
DB 121 VSS 123

RESULT 15  
ID ABP44313 standard; protein; 249 AA.  
XX  
XX ABP44313;  
AC  
XX  
XX 19-AUG-2002 (first entry)  
DT Human Blys binding scFv SEQ ID 324.  
XX  
XX  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX Homo sapiens.  
XX WO200202641-A1.  
XX  
XX 10-JAN-2002.  
XX  
XX 15-JUN-2001; 2001WO-US019110.  
XX  
XX 16-JUN-2000; 2000US-0212210P.  
XX 17-OCT-2000; 2000US-0240816P.  
XX 16-MAR-2001; 2001US-0276248P.  
XX 21-MAR-2001; 2001US-0277379P.  
XX 25-MAY-2001; 2001US-0293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
XX diagnosis and treatment of cancers and immune disorders.  
XX  
XX Claim 1, Page 790-791; 3148pp; English.  
XX  
XX This invention describes novel antibodies that immunospecifically bind to  
XX B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
XX tumour necrosis factor (TNF) super family and induces B cell  
XX proliferation and differentiation. The antibodies of the invention have  
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
XX antirheumatic and antiAIDS activity and can be used in vaccines to  
XX inhibit the expression and activity of Blys. The antibodies bind to Blys  
XX and so may be used to detect and quantitate the presence of Blys in  
XX biological samples and may be used in this way to diagnose disease  
XX associated with aberrant expression of Blys. They may also be  
XX administered to treat diseases associated with aberrant Blys expression  
XX and activity such as cancer, immune, and autoimmune disorders and  
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
XX the antibodies and fragments of the antibodies described in the method of  
XX the invention  
XX  
XX Sequence 249 AA;  
SQ  
Query Match 98.8%; Score 632; DB 5; Length 249;  
Best Local Similarity 98.4%; Pred. No. 5.5e-51;  
Matches 121; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVQLQSGAEVKKRPGSSVRVSCAKSGCTFNNAIMNVRQAPQGLEWMGCIIPMFCTAKY 60  
DB 1 QVQLQSGAEVKKRPGSSVRVSCAKSGCTFNNAIMNVRQAPQGLEWMGCIIPMFCTAKY 60

Qy	61	SONFOGRVAITADESTSTASMEISIRSEDTAVYTCARSRDILLPPHGMVDWGRGTMYT	120
Db	61	SONFOGRVAITADESTSTASMEISIRSEDTAVYTCARSRDILLPPHGMVDWGRGTMYT	120
Qy	121	VSS 123	
Db	121	VSS 123	

Search completed: September 9, 2004, 11:06:30  
Job time : 54.0897 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: September 9, 2004, 11:04:55 : Search time 15.7692 Seconds  
(without alignments)  
402.683 Million cell updates/sec

Title: US-09-880-748-2\_COPY\_1\_123

Perfect score: 640  
Sequence: 1 QVQLQSGAEVKKPGSSVRV.....LRFHYGMDVGRGTWTVSS 123

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

1 number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 70 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/iaa/6C\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	502	78.4	123	2	US-08-652-816A-8 Sequence 8, Appl
2	501	78.3	123	2	US-08-652-816A-1 Sequence 9, Appl
3	499	78.0	123	2	US-08-652-816A-9 Sequence 21, Appl
4	496	77.5	119	4	US-09-025-769B-21 Sequence 6, Appl
5	494	77.2	123	2	US-08-652-816A-6 Sequence 35, Appl
6	491.5	76.8	120	4	US-09-025-769B-35 Sequence 7, Appl
7	491.5	76.8	120	4	US-09-025-769B-57 Sequence 10, Appl
8	483	75.5	123	2	US-08-652-816A-7 Sequence 12, Appl
9	469	73.3	147	1	US-08-378-939-10 Sequence 4, Appl
10	465.5	72.7	147	1	US-08-217-918-4 Sequence 12, Appl
11	462	72.2	120	2	US-08-428-197-12 Sequence 12, Appl
12	462	72.2	120	5	PCT-US93-10555-12 Sequence 12, Appl
13	458	71.6	121	2	US-08-332-081B-41 Sequence 13, Appl
14	456	71.2	120	2	US-08-428-197-13 Sequence 13, Appl
15	456	71.2	120	5	PCT-US93-10555-13 Sequence 50, Appl
16	453	70.8	119	3	US-08-983-607-50 Sequence 2, Appl
17	432	67.5	123	1	PCT-US95-00067-2 Sequence 53, Appl
18	430	67.2	123	1	US-08-482-882-53 Sequence 53, Appl
19	430	67.2	123	2	US-08-483-389-53 Sequence 53, Appl
20	430	67.2	123	2	US-08-487-113D-53 Sequence 53, Appl
21	430	67.2	123	2	US-08-473-503-53 Sequence 53, Appl
22	430	67.2	123	2	US-08-483-932-53 Sequence 53, Appl
23	430	67.2	123	2	US-08-720-420A-53 Sequence 53, Appl
24	430	67.2	123	3	US-08-714-017-53 Sequence 53, Appl
25	430	67.2	123	3	US-08-475-680-53 Sequence 3, Appl
26	429.5	67.1	128	4	US-08-635-109-3 Sequence 19, Appl
27	427.5	66.8	139	1	US-08-253-877C-19 Sequence 19, Appl

28	427.5	66.8	139	2	US-08-452-164A-19 Sequence 19, Appl
29	427.5	66.8	139	3	US-08-603-024-18 Sequence 18, Appl
30	427.5	66.8	139	4	US-08-450-809-14 Sequence 14, Appl
31	427	66.7	117	1	US-07-634-278-4 Sequence 4, Appl
32	427	66.7	117	1	US-07-634-278-15 Sequence 15, Appl
33	427	66.7	117	1	US-07-634-278-72 Sequence 72, Appl
34	427	66.7	117	1	US-07-634-278-104 Sequence 104, Appl
35	427	66.7	117	1	US-08-477-728-4 Sequence 4, Appl
36	427	66.7	117	1	US-08-477-728-15 Sequence 15, Appl
37	427	66.7	117	1	US-08-477-728-72 Sequence 72, Appl
38	427	66.7	117	1	US-08-477-728-104 Sequence 104, Appl
39	427	66.7	117	1	US-08-474-040-4 Sequence 4, Appl
40	427	66.7	117	1	US-08-474-040-15 Sequence 15, Appl
41	427	66.7	117	1	US-08-474-040-72 Sequence 72, Appl
42	427	66.7	117	1	US-08-474-040-104 Sequence 104, Appl
43	427	66.7	117	1	US-08-487-200-4 Sequence 4, Appl
44	427	66.7	117	1	US-08-487-200-15 Sequence 15, Appl
45	427	66.7	117	1	US-08-487-200-72 Sequence 72, Appl
46	427	66.7	117	1	US-08-487-200-104 Sequence 104, Appl
47	427	66.7	117	1	US-08-488-113B-166 Sequence 166, Appl
48	427	66.7	117	1	US-08-477-484B-166 Sequence 166, Appl
49	427	66.7	117	1	US-08-107-663D-52 Sequence 52, Appl
50	427	66.7	117	1	US-08-472-788A-52 Sequence 52, Appl
51	427	66.7	117	2	US-08-477-531B-52 Sequence 52, Appl
52	427	66.7	117	2	US-08-646-360-166 Sequence 166, Appl
53	427	66.7	117	2	US-08-082-842A-52 Sequence 52, Appl
54	427	66.7	117	3	US-08-839-765-166 Sequence 166, Appl
55	427	66.7	117	3	US-09-136-389-166 Sequence 166, Appl
56	427	66.7	117	3	US-08-484-537-15 Sequence 15, Appl
57	427	66.7	117	3	US-08-484-537-72 Sequence 72, Appl
58	427	66.7	117	3	US-08-484-537-104 Sequence 104, Appl
59	427	66.7	117	4	US-09-450-520A-13 Sequence 13, Appl
60	427	66.7	117	4	US-09-711-483B-166 Sequence 166, Appl
61	427	66.7	117	4	US-09-711-483B-166 Sequence 166, Appl
62	427	66.7	117	4	US-08-202-047-22 Sequence 22, Appl
63	426.5	66.6	128	3	US-08-964-690-22 Sequence 22, Appl
64	426.5	66.6	128	3	PCT-US93-11611-7 Sequence 7, Appl
65	426	66.6	129	2	US-08-561-521-45 Sequence 45, Appl
66	426	66.6	129	4	US-08-525-539A-77 Sequence 77, Appl
67	426	66.6	129	5	PCT-US95-01219-45 Sequence 45, Appl
68	426	66.6	125	3	US-09-199-149-3 Sequence 3, Appl
69	423	66.1	139	4	US-09-355-925-8 Sequence 8, Appl
70	422.5	66.0	139	4	US-09-355-925-8 Sequence 8, Appl

## ALIGNMENTS

RESULT 1  
US-08-652-816A-8  
Sequence 8, Application US/08652816A  
Patent No. 5872215  
GENERAL INFORMATION:  
APPLICANT: Oshbourn, JK  
APPLICANT: Allen, DJ  
TITLE OF INVENTION: Specific binding members, materials and  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,816A  
FILING DATE: 23-MAY-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.4  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.8  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 23-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9525004.9  
FILING DATE: 07-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9610824.6  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/02240  
FILING DATE: 02-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/244,597  
FILING DATE: 01-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/33308  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-652-816A-8

Query Match 78.4%; Score 502; DB 2; Length 123;  
Best Local Similarity 79.7%; Pred. No. 1.8e-44;  
Matches 98; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVQLQSGAEVKKPSSSVRVSCKASGTFNNNAINMVRQAPQGLPMGSIIPMFGTAKY 60  
DB 1 QVQLVSGAEVKKPSSSVKSCASGTSNINMLRQAPQGLPMGSIIPSGTANY 60  
QY 61 SONFGQRAVITADESTSTASMLSLRSEDTAVYYCARSDLLLPHYGMDVWGRTMY 120  
61 AQKFGRLTITADESTSTAYMELSLRSEDTAVYYCARHNHNYELYYVMDVWGQGTMY 120  
QY 121 VSS 123  
DB 121 VSS 123

RESULT 2  
US-08-652-816A-1  
Sequence 1, Application US/08652816A  
Patent No. 5872215

GENERAL INFORMATION:  
APPLICANT: Osbourn, JK  
APPLICANT: Allen, DJ  
APPLICANT: McCafferty, JG  
TITLE OF INVENTION: Specific binding members, materials and  
TITLE OF INVENTION: methods.  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,816A  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.4  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.8  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 23-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9525004.9  
FILING DATE: 07-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9610824.6  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/02240  
FILING DATE: 02-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/244,597  
FILING DATE: 01-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/33308  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-652-816A-1

Query Match 78.3%; Score 501; DB 2; Length 123;  
Best Local Similarity 80.6%; Pred. No. 2.3e-44;  
Matches 100; Conservative 10; Mismatches 12; Indels 2; Gaps 2;

QY 1 QVQLQSGAEVKKPSSSVRVSCKASGTFNNNAINMVRQAPQGLPMGSIIPMFGTAKY 60  
DB 1 QVQLVSGAEVKKPSSSVKSCASGTSNINMLRQAPQGLPMGSIIPSGTANY 60  
QY 61 SONFGQRAVITADESTSTASMLSLRSEDTAVYYCA-RSRDLLLPHYGMDVWGRTMY 119  
61 AQKFGRLTITADESTSTAYMELSLRSEDTAVYYCAGSHNYELY-YVMDVWGQGTMY 119  
QY 120 TVSS 123  
DB 120 TVSS 123

RESULT 3  
US-08-652-816A-9

Sequence 9, Application US/08652816A  
Patent No. 5872215  
GENERAL INFORMATION:  
APPLICANT: Osbourn, JK  
APPLICANT: Allen, DJ  
APPLICANT: McCafferty, JG  
TITLE OF INVENTION: Specific binding members, materials and  
TITLE OF INVENTION: methods.  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,816A  
FILING DATE: 23-MAY-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.4  
FILING DATE: 02-DEC-1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.8  
FILING DATE: 02-DEC-1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 23-SEP-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9525004.9  
FILING DATE: 07-DEC-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9610824.6  
FILING DATE: 23-MAY-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/02240  
FILING DATE: 02-DEC-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/244,597  
FILING DATE: 01-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/33308  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-652-816A-9

Query Match 78.0%; Score 499; DB 2; Length 123;  
Best Local Similarity 80.6%; Pred. No. 3.7e-44;  
Matches 100; Conservative 9; Mismatches 13; Indels 2; Gaps 2;

QY 1 QVQLQSGAEVKKPGSSVRVSCKASGCTFNNAIINWVROAPQCGLEMMGIIIPMGSTAKY 60  
DB 1 QVQLVQSGAEVKKPGSSVRVSCKASGCTFNNAIINWVROAPQCGLEMMGIIIPMGSTAKY 60  
QY 61 SQNFGRAVITADESTSTASMEISLRSEDTAVYYCA-RSRDLLFPYHGMVGRGTAV 119  
DB 61 AKKFGRLTITADESTSTASMEISLRSEDTAVYYCA-RSRDLLFPYHGMVGRGTAV 119  
QY 120 TVSS 123  
DB 120 TVSS 123

RESULT 4  
US-09-025-769B-21  
Sequence 21, Application US/09025769B  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter

APPLICANT: Ilaq, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckhuhn, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-21

Query Match 77.5%; Score 496; DB 4; Length 119;  
Best Local Similarity 79.2%; Pred. No. 7.2e-44;  
Matches 99; Conservative 9; Mismatches 9; Indels 8; Gaps 2;

QY 1 QVQLQSGAEVKKPGSSVRVSCKASGCTFNNAIINWVROAPQCGLEMMGIIIPMGSTAKY 60  
DB 1 QVQLVQSGAEVKKPGSSVRVSCKASGCTFNNAIINWVROAPQCGLEMMGIIIPMGSTAKY 60  
QY 61 SQNFGRAVITADESTSTASMEISLRSEDTAVYYCARSDLLFPYHGMVGRGTAV 118  
DB 61 AKKFGRLTITADESTSTASMEISLRSEDTAVYYCARSDLLFPYHGMVGRGTAV 114  
QY 119 TVSS 123  
DB 115 TVSS 119

RESULT 5  
US-08-652-816A-6  
Sequence 6, Application US/08652816A  
Patent No. 5872215  
GENERAL INFORMATION:  
APPLICANT: Osbourn, JK  
APPLICANT: Allen, DJ  
APPLICANT: McCafferty, JG  
TITLE OF INVENTION: Specific binding members, materials and  
TITLE OF INVENTION: methods.  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Bornum  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois

COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,816A  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.4  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.8  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 23-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9525004.9  
FILING DATE: 07-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9610824.6  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/02240  
FILING DATE: 02-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/244,597  
FILING DATE: 01-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/33308  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-652-816A-6

Query Match 77.2%; Score 494; DB 2; Length 123;  
Best Local Similarity 78.9%; Pred. No. 1.2e-43;  
Matches 97; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 1 QVQLQSGAEVKKPSSVSVCASGCTFNNAIMVVRQAPGGGLMMGGIIIPMEGTAKY 60  
DB 1 QVQLVDSGAEVKKPSSVSVCASGCTFSNSIFIMLRQAPGGGLMMGGIIIPSGETANY 60

QY 61 SQNFGRAVITADESTSTASMEISLSRSEDVAVYYCARSDLLFPHYGMDVWGRTMT 120  
DB 61 AQKFGRLTITADESTSTAYMELSLRSEDVAVYYCARSHNYELYYIMDVWGQGTMT 120

QY 121 VSS 123  
DB 121 VSS 123

RESULT 6  
US-09-025-769B-35  
Sequence 35, Application US/09025769B  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon

APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-35

Query Match 76.8%; Score 491.5; DB 4; Length 120;  
Best Local Similarity 79.8%; Pred. No. 2.1e-43;  
Matches 99; Conservative 8; Mismatches 12; Indels 5; Gaps 2;

QY 1 QVQLQSGAEVKKPSSVSVCASGCTFNNAIMVVRQAPGGGLMMGGIIIPMEGTAKY 60  
DB 1 QVQLVDSGAEVKKPSSVSVCASGCTFSNSIFIMLRQAPGGGLMMGGIIIPSGETANY 60

QY 61 SQNFGRAVITADESTSTASMEISLSRSEDVAVYYCARSDLLFPHYGMDVWGRTMT 119  
DB 61 AQKFGRLTITADESTSTAYMELSLRSEDVAVYYCARWGD---GFYAMDVWGQGTIV 116

QY 120 TVSS 123  
DB 117 TVSS 120

RESULT 7  
US-09-025-769B-57  
Sequence 57, Application US/09025769B  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA

ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-57

Query Match 76.8%; Score 491.5; DB 4; Length 120;  
Best Local Similarity 79.8%; Pred. No. 2.1e-43;  
Matches 99; Conservative 8; Mismatches 12; Indels 5; Gaps 2;

QY 1 QVQLQSGAEVKKRQPSVSVSCASGCTFNNAIMNVRQAPQGLEMGGIIPMGTAY 60  
DB 1 QVQLVSGAEVKKRQPSVSVSCASGCTFSVAISVVRQAPQGLEMGGIIPFGTANY 60  
QY 61 SONFGQVAITADESTSTASMEISLRSEDTAVYYCAR-SRDLLRPHYGMVDWGRGTNY 119  
DB 61 AQKFGRLITTADESTSTAYMELSLRSEDTAVYYCAGARGD---GFAMDWGGGTIV 116  
QY 120 TVSS 123  
DB 117 TVSS 120

RESULT 8  
US-08-652-816A-7  
Sequence 7, Application US/08652816A  
Patent No. 5872215  
GENERAL INFORMATION:  
APPLICANT: Oebourn, JK  
APPLICANT: Allen, DJ  
TITLE OF INVENTION: Specific binding members, materials and  
TITLE OF INVENTION: method.  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,816A  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.4  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9125579.8  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 23-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9525004.9  
FILING DATE: 07-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9610824.6  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/02240  
FILING DATE: 02-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/244,597  
FILING DATE: 01-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/33308  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-652-816A-7

Query Match 75.5%; Score 483; DB 2; Length 123;  
Best Local Similarity 78.0%; Pred. No. 1.6e-42;  
Matches 96; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 QVQLQSGAEVKKRQPSVSVSCASGCTFNNAIMNVRQAPQGLEMGGIIPMGTAY 60  
DB 1 QVQLVSGAEVKKRQPSVSVSCASGCTFSNSPIMLRQAPQGLEMGGIIPFGTANY 60  
QY 61 SONFGQVAITADESTSTASMEISLRSEDTAVYYCARSRDLLRPHYGMVDWGRGTNY 120  
DB 61 AQKFGRLITTADESTSTAYMELSLRSEDTAVYYCAGANSCNRSYVVYMDVRGGGTIVT 120  
QY 121 VSS 123  
DB 121 VSS 123

RESULT 9  
US-08-378-939-10  
Sequence 10, Application US/08378939  
Patent No. 5876961  
GENERAL INFORMATION:  
APPLICANT: CROME, JAMES SCOTT  
APPLICANT: LEWIS, ALAN PETER  
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ  
STREET: 555 THIRTEENTH ST. N.W.  
CITY: WASHINGTON  
STATE: D. C.  
COUNTRY: U.S.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,939

```

; LENGTH: 147 amino acids
; TYPE: amino acid

```

Query Match	Score
72.28;	

Query Match      72.2%;    Score 462;    DB 2;    Length 120;



Best Local Similarity 74.0%; Pred. No. 2, 3e-40;  
Matches 91; Conservative 14; Mismatches 14; Indels 4; Gaps 2;

QY 2 VOLQSGAEVKKRGSSSVKRVSCKASGTFNNNAIMVROAPGQGLMGGIIPFGTAKYS 61  
DB 1 VOLVQSGAEVKKRGSSSVKRVCKASGDTFSSAISWROAPGQGLMGGIIPFGPNYA 60

QY 62 QNFQGRVAITADESTASTMELSLRSEDTAVYCAR-SRDLLPFPHYGMDVWGRTMYT 120  
DB 61 QNFQGRVITTTDESTASTMELSLRSEDTALYYCARBGRMAINP---FDYWGQGLVYT 117

QY 121 VSS 123  
DB 118 VSS 120

RESULT 12  
PCT-US93-10555-12

Sequence 12, Application PC/TUS9310555.  
GENERAL INFORMATION:

APPLICANT: SILVERMAN, GREGG J.

TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF

TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH

TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Spensley Horn Jubas & Lubitz

STREET: 1880 Century Park East - Suite 500

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/10555

FILING DATE: 29-OCT-1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Howells, Stacy L.

REGISTRATION/DOCKET NUMBER: 34,842

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5110

TELEFAX: (619) 455-5110

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

CLONE: BOR

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..120

PCT-US93-10555-12

Query Match

Best Local Similarity 74.0%; Score 462; DB 5; Length 120;

Matches 91; Conservative 14; Mismatches 14; Indels 4; Gaps 2;

QY 2 VOLQSGAEVKKRGSSSVKRVSCKASGTFNNNAIMVROAPGQGLMGGIIPFGTAKYS 61  
DB 1 VOLVQSGAEVKKRGSSSVKRVCKASGDTFSSAISWROAPGQGLMGGIIPFGPNYA 60

QY 62 QNFQGRVAITADESTASTMELSLRSEDTAVYCAR-SRDLLPFPHYGMDVWGRTMYT 120  
DB 61 QNFQGRVITTTDESTASTMELSLRSEDTALYYCARBGRMAINP---FDYWGQGLVYT 117

DB 61 QNFQGRVITTTDESTASTMELSLRSEDTALYYCARBGRMAINP---FDYWGQGLVYT 117

QY 121 VSS 123  
DB 118 VSS 120

RESULT 13  
US-08-232-081B-41

Sequence 41, Application US/08232081B  
Patent No. 5886152

GENERAL INFORMATION:

APPLICANT: NAKATANI, TOMOYUKI

APPLICANT: GOMI, HIDEYUKI

APPLICANT: WIDENES, JOHN

APPLICANT: NOGUCHI, HIROSHI

TITLE OF INVENTION: HUMANIZED B-B10

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESSES:

ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH

STREET: PO BOX 747

CITY: FALLS CHURCH

STATE: VA

COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,081B

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: SVENSSON, LEONARD R

REGISTRATION/DOCKET NUMBER: 30,330

REFERENCE/DOCKET NUMBER: 20-3484

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:

LENGTH: 121 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-232-081B-41

Query Match

Best Local Similarity 71.6%; Score 458; DB 2; Length 121;

Matches 90; Conservative 14; Mismatches 15; Indels 6; Gaps 2;

QY 1 QVOLQSGAEVKKRGSSSVKRVSCKASGTFNNNAIMVROAPGQGLMGGIIPFGTAKY 60  
DB 1 EYHLVQSGAEVKKRGSSSVKRVCKASGDTFSSAISWROAPGQGLMGGIIPFGPNYA 60

QY 61 SQNFQGRVAITADESTASTMELSLRSEDTAVYCAR-SRDLLPFPHYG-MDVWGRTMY 118  
DB 61 AQNFQGRVITTTDESTASTMELSLRSEDTALYYCARBGRMAINP---YGDYGRPDPFGQGLT 116

QY 119 VTVSS 123  
DB 117 VTVSS 121

RESULT 14  
US-08-428-197-13

Sequence 13, Application US/08428197

Patent No. 5891438

GENERAL INFORMATION:

APPLICANT: SILVERMAN, GREGG J.

TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF ANTIBODIES THROUGH  
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED  
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPRANANTIGEN AND CONJUGATES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East - Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/428,197  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10555  
FILING DATE: 29-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Howells, Stacy L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: FD-2630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: KAS  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..120  
US-08-428-197-13

Query Match 71.2%; Score 456; DB 2; Length 120;  
Best Local Similarity 72.6%; Pred. No. 9.6e-40;  
Matches 90; Conservative 13; Mismatches 15; Indels 6; Gaps 2;

Db 2 VOLQSGAEVKKPSSSVRSCKASGCTFNNAIMWVROAPGQGLEWVGIIIPMGSTAKYS 61  
1 VHLVQSGAEVKKPSSSVRSCKASGCTFSSVYALSWRQAPGQGLEWVGIIIPFGQANYA 60

QY 62 QNPGRAVITADESTSTASMELSLRSDPTAVYCARSDLLPFHYG--MDVWGRGTWV 119  
61 QKFGRAVITADESTSTASMELSLRSDPTAVYCARSDLLPFHYG---YDYGRRPDPFGQGLIV 116

Db 120 TVSS 123  
117 TVSS 120

QY 120 TVSS 123  
117 TVSS 120

RESULT 15  
PCT-US93-10555-13  
Sequence 13, Application PC/TUS9310555  
GENERAL INFORMATION:  
APPLICANT: SILVERMAN GREGG J.  
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF  
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH  
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPRANANTIGEN AND CONJUGATES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East - Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10555  
FILING DATE: 29-OCT-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Howells, Stacy L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: FD-2630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: KAS  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..120  
PCT-US93-10555-13

Query Match 71.2%; Score 456; DB 5; Length 120;  
Best Local Similarity 72.6%; Pred. No. 9.6e-40;  
Matches 90; Conservative 13; Mismatches 15; Indels 6; Gaps 2;

QY 2 VOLQSGAEVKKPSSSVRSCKASGCTFNNAIMWVROAPGQGLEWVGIIIPMGSTAKYS 61  
1 VHLVQSGAEVKKPSSSVRSCKASGCTFSSVYALSWRQAPGQGLEWVGIIIPFGQANYA 60

Db 62 QNPGRAVITADESTSTASMELSLRSDPTAVYCARSDLLPFHYG--MDVWGRGTWV 119  
61 QKFGRAVITADESTSTASMELSLRSDPTAVYCARSDLLPFHYG---YDYGRRPDPFGQGLIV 116

QY 120 TVSS 123  
117 TVSS 120

Db 120 TVSS 123  
117 TVSS 120

Search completed: September 9, 2004, 11:09:18  
Job time: 16.7692 secs

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OM protein - protein search, using sw model

Run on: September 9, 2004, 11:07:30 ; Search time 90.4103 Seconds

(without alignments)  
436.287 Million cell updates/sec

Title: US-09-880-748-2\_COPY\_1\_123

Perfect score: 640  
Sequence: 1 OVQLQSGAEVKKFGSSVRV.....LPPHYGMDVGRGNTVTS 123

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

1 number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 70 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubppa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubppa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubppa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubppa/US09\_NEW\_PUB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubppa/US10\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubppa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	640	100.0	246	10	US-09-880-748-928 Sequence 928, App
2	640	100.0	246	12	US-10-293-418-928 Sequence 928, App
3	640	100.0	249	10	US-09-880-748-2 Sequence 2, Appli
4	640	100.0	249	10	US-09-880-748-471 Sequence 471, App
5	640	100.0	249	10	US-09-880-748-479 Sequence 479, App
6	640	100.0	249	10	US-09-880-748-618 Sequence 618, App
7	640	100.0	249	10	US-09-880-748-719 Sequence 719, App
8	640	100.0	249	10	US-09-880-748-796 Sequence 796, App
9	640	100.0	249	12	US-10-293-418-2 Sequence 2, Appli
10	640	100.0	249	12	US-10-293-418-471 Sequence 471, App
11	640	100.0	249	12	US-10-293-418-479 Sequence 479, App
12	640	100.0	249	12	US-10-293-418-618 Sequence 618, App
13	640	100.0	249	12	US-10-293-418-719 Sequence 719, App
14	640	100.0	249	12	US-10-293-418-796 Sequence 796, App
15	637	99.5	246	10	US-09-880-748-1426 Sequence 1426, Ap

#### ALIGNMENTS

16	637	99.5	246	10	US-09-880-748-1781	Sequence 1781, Ap
17	637	99.5	246	12	US-10-293-418-1426	Sequence 1426, Ap
18	637	99.5	246	12	US-10-293-418-1781	Sequence 1781, Ap
19	637	99.5	249	10	US-09-880-748-613	Sequence 613, App
20	637	99.5	249	12	US-10-293-418-613	Sequence 613, App
21	634	99.1	249	10	US-09-880-748-659	Sequence 659, App
22	634	99.1	249	10	US-09-880-748-1748	Sequence 1748, Ap
23	634	99.1	249	12	US-10-293-418-659	Sequence 659, App
24	634	99.1	249	12	US-10-293-418-1748	Sequence 1748, Ap
25	633	98.9	246	10	US-09-880-748-1308	Sequence 1308, Ap
26	633	98.9	246	12	US-10-293-418-1308	Sequence 1308, Ap
27	632	98.8	249	10	US-09-880-748-324	Sequence 324, App
28	632	98.8	249	10	US-09-880-748-688	Sequence 688, App
29	632	98.8	249	12	US-10-293-418-324	Sequence 324, App
30	632	98.8	249	12	US-10-293-418-688	Sequence 688, App
31	631	98.6	246	10	US-09-880-748-1818	Sequence 1818, Ap
32	631	98.6	246	12	US-10-293-418-1818	Sequence 1818, Ap
33	631	98.6	249	10	US-09-880-748-721	Sequence 721, App
34	631	98.6	249	12	US-10-293-418-721	Sequence 721, App
35	626	97.8	249	10	US-09-880-748-786	Sequence 786, App
36	626	97.8	249	10	US-09-880-748-794	Sequence 794, App
37	626	97.8	249	10	US-09-880-748-804	Sequence 804, App
38	626	97.8	249	12	US-10-293-418-786	Sequence 786, App
39	626	97.8	249	12	US-10-293-418-794	Sequence 794, App
40	626	97.8	249	12	US-10-293-418-804	Sequence 804, App
41	623	97.3	249	10	US-09-880-748-325	Sequence 325, App
42	623	97.3	249	10	US-09-880-748-761	Sequence 761, App
43	623	97.3	249	10	US-09-880-748-815	Sequence 815, App
44	623	97.3	249	12	US-10-293-418-325	Sequence 325, App
45	623	97.3	249	12	US-10-293-418-761	Sequence 761, App
46	623	97.3	249	10	US-09-880-748-815	Sequence 815, App
47	621	97.0	249	10	US-09-880-748-332	Sequence 332, App
48	621	97.0	249	10	US-09-880-748-329	Sequence 329, App
49	621	97.0	249	10	US-09-880-748-461	Sequence 461, App
50	621	97.0	249	10	US-09-880-748-744	Sequence 744, App
51	621	97.0	249	10	US-09-880-748-752	Sequence 752, App
52	621	97.0	249	10	US-09-880-748-774	Sequence 774, App
53	621	97.0	249	10	US-09-880-748-792	Sequence 792, App
54	621	97.0	249	10	US-09-880-748-797	Sequence 797, App
55	621	97.0	249	10	US-09-880-748-808	Sequence 808, App
56	621	97.0	249	10	US-09-880-748-811	Sequence 811, App
57	621	97.0	249	10	US-09-880-748-825	Sequence 825, App
58	621	97.0	249	10	US-09-880-748-826	Sequence 826, App
59	621	97.0	249	12	US-10-293-418-322	Sequence 322, App
60	621	97.0	249	12	US-10-293-418-329	Sequence 329, App
61	621	97.0	249	12	US-10-293-418-461	Sequence 461, App
62	621	97.0	249	12	US-10-293-418-744	Sequence 744, App
63	621	97.0	249	12	US-10-293-418-752	Sequence 752, App
64	621	97.0	249	12	US-10-293-418-774	Sequence 774, App
65	621	97.0	249	12	US-10-293-418-792	Sequence 792, App
66	621	97.0	249	12	US-10-293-418-797	Sequence 797, App
67	621	97.0	249	12	US-10-293-418-808	Sequence 808, App
68	621	97.0	249	12	US-10-293-418-811	Sequence 811, App
69	621	97.0	249	12	US-10-293-418-825	Sequence 825, App
70	621	97.0	249	12	US-10-293-418-826	Sequence 826, App

RESULT 1  
US-09-880-748-928  
Sequence 928, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly5  
; FILE REFERENCE: PFS23  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816

;; PRIOR FILING DATE: 2000-10-17  
;; PRIOR APPLICATION NUMBER: 60/276,248  
;; PRIOR FILING DATE: 2001-03-16  
;; PRIOR APPLICATION NUMBER: 60/277,379  
;; PRIOR FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/293,499  
;; PRIOR FILING DATE: 2001-05-25  
;; NUMBER OF SEQ ID NOS: 3239  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO: 928  
;; LENGTH: 246  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-880-748-928

Query Match 100.0%; Score 640; DB 10; Length 246;  
Best Local Similarity 100.0%; Pred. No. 8,7e-57;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QVQLOOSGAIEVKKPGSSVRSVSCASGCTFNNAIINWROAPQGLEWNGIIPMFETAKY 60  
1 QVQLOOSGAIEVKKPGSSVRSVSCASGCTFNNAIINWROAPQGLEWNGIIPMFETAKY 60  
61 SONFOGRAVITADESTSTASMEISLRSEDTAVYYCARSDLLLPHYGMDVWGRTMYT 120  
61 SONFOGRAVITADESTSTASMEISLRSEDTAVYYCARSDLLLPHYGMDVWGRTMYT 120  
121 VSS 123  
121 VSS 123  
Db 121 VSS 123

RESULT 2  
US-10-293-418-928  
; Sequence 928, Application US/10293418  
; Publication No. US20030223996A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PFS23P2  
; CURRENT APPLICATION NUMBER: US/10/293,418  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO: 928  
; LENGTH: 246  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-928

Query Match 100.0%; Score 640; DB 12; Length 246;  
Best Local Similarity 100.0%; Pred. No. 8,7e-57;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QVQLOOSGAIEVKKPGSSVRSVSCASGCTFNNAIINWROAPQGLEWNGIIPMFETAKY 60  
1 QVQLOOSGAIEVKKPGSSVRSVSCASGCTFNNAIINWROAPQGLEWNGIIPMFETAKY 60  
61 SONFOGRAVITADESTSTASMEISLRSEDTAVYYCARSDLLLPHYGMDVWGRTMYT 120  
61 SONFOGRAVITADESTSTASMEISLRSEDTAVYYCARSDLLLPHYGMDVWGRTMYT 120  
121 VSS 123  
121 VSS 123  
Db 121 VSS 123

QY 61 SONFOGRAVITADESTSTASMEISLRSEDTAVYYCARSDLLLPHYGMDVWGRTMYT 120  
DB 61 SONFOGRAVITADESTSTASMEISLRSEDTAVYYCARSDLLLPHYGMDVWGRTMYT 120  
QY 121 VSS 123  
DB 121 VSS 123

RESULT 3  
US-09-880-748-2  
; Sequence 2, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PFS23  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 2  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2

Query Match 100.0%; Score 640; DB 10; Length 249;  
Best Local Similarity 100.0%; Pred. No. 8,8e-57;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QVQLOOSGAIEVKKPGSSVRSVSCASGCTFNNAIINWROAPQGLEWNGIIPMFETAKY 60  
1 QVQLOOSGAIEVKKPGSSVRSVSCASGCTFNNAIINWROAPQGLEWNGIIPMFETAKY 60  
61 SONFOGRAVITADESTSTASMEISLRSEDTAVYYCARSDLLLPHYGMDVWGRTMYT 120  
61 SONFOGRAVITADESTSTASMEISLRSEDTAVYYCARSDLLLPHYGMDVWGRTMYT 120  
121 VSS 123  
121 VSS 123  
Db 121 VSS 123

RESULT 4  
US-09-880-748-471  
; Sequence 471, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PFS23  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 471  
LENGTH: 249  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-880-748-471

Query Match 100.0%; Score 640; DB 10; Length 249;  
Best Local Similarity 100.0%; Pred. No. 8.8e-57;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLOOQSGAEVKKPGSSVRVSCKASGCTFNNNAINWVROAPGQGLEMMGIIIMPGTAKY 60  
DB 1 QVLOOQSGAEVKKPGSSVRVSCKASGCTFNNNAINWVROAPGQGLEMMGIIIMPGTAKY 60  
QY 61 SQNFGQRAVITADESTSTASMEISLRSEDTAVYYCARSRDILLFPHYGMDVWGRTMT 120  
61 SQNFGQRAVITADESTSTASMEISLRSEDTAVYYCARSRDILLFPHYGMDVWGRTMT 120  
QY 121 VSS 123  
DB 121 VSS 123

RESULT 5  
US-09-880-748-479

Sequence 479, Application US/09880748  
Publication No. US20030059937A1  
GENERAL INFORMATION:

APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PF523  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 479  
LENGTH: 249  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-880-748-479

Query Match 100.0%; Score 640; DB 10; Length 249;  
Best Local Similarity 100.0%; Pred. No. 8.8e-57;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLOOQSGAEVKKPGSSVRVSCKASGCTFNNNAINWVROAPGQGLEMMGIIIMPGTAKY 60  
DB 1 QVLOOQSGAEVKKPGSSVRVSCKASGCTFNNNAINWVROAPGQGLEMMGIIIMPGTAKY 60  
QY 61 SQNFGQRAVITADESTSTASMEISLRSEDTAVYYCARSRDILLFPHYGMDVWGRTMT 120  
61 SQNFGQRAVITADESTSTASMEISLRSEDTAVYYCARSRDILLFPHYGMDVWGRTMT 120  
QY 121 VSS 123  
DB 121 VSS 123

RESULT 6  
US-09-880-748-618

Sequence 618, Application US/09880748  
Publication No. US20030059937A1  
GENERAL INFORMATION:

APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PF523  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 618  
LENGTH: 249  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-880-748-618

Query Match 100.0%; Score 640; DB 10; Length 249;  
Best Local Similarity 100.0%; Pred. No. 8.8e-57;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLOOQSGAEVKKPGSSVRVSCKASGCTFNNNAINWVROAPGQGLEMMGIIIMPGTAKY 60  
DB 1 QVLOOQSGAEVKKPGSSVRVSCKASGCTFNNNAINWVROAPGQGLEMMGIIIMPGTAKY 60  
QY 61 SQNFGQRAVITADESTSTASMEISLRSEDTAVYYCARSRDILLFPHYGMDVWGRTMT 120  
61 SQNFGQRAVITADESTSTASMEISLRSEDTAVYYCARSRDILLFPHYGMDVWGRTMT 120  
QY 121 VSS 123  
DB 121 VSS 123

RESULT 7  
US-09-880-748-719

Sequence 719, Application US/09880748  
Publication No. US20030059937A1  
GENERAL INFORMATION:

APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PF523  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 719  
LENGTH: 249  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-880-748-719

Query Match 100.0%; Score 640; DB 10; Length 249;  
Best Local Similarity 100.0%; Pred. No. 8.8e-57;

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Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVQLQSGAEVKKPGSSVRVSCASGCTFNNAIINWVROAPGQGLEWMGGIIPMFETAKY 60
  |||
  1 QVQLQSGAEVKKPGSSVRVSCASGCTFNNAIINWVROAPGQGLEWMGGIIPMFETAKY 60
Db 61 SQNFGRAVITADESTSTASMSLSLRSEDTAVYYCARSRDLLFPHYGMDVWGRTMT 120
  |||
  61 SQNFGRAVITADESTSTASMSLSLRSEDTAVYYCARSRDLLFPHYGMDVWGRTMT 120
QY 121 VSS 123
  |||
  121 VSS 123
Db 121 VSS 123

RESULT 8
US-09-880-748-796
; Sequence 796, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 796
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-796

Query Match 100.0%; Score 640; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 8.8e-57;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  1 QVQLQSGAEVKKPGSSVRVSCASGCTFNNAIINWVROAPGQGLEWMGGIIPMFETAKY 60
  |||
  1 QVQLQSGAEVKKPGSSVRVSCASGCTFNNAIINWVROAPGQGLEWMGGIIPMFETAKY 60
QY 61 SQNFGRAVITADESTSTASMSLSLRSEDTAVYYCARSRDLLFPHYGMDVWGRTMT 120
  |||
  61 SQNFGRAVITADESTSTASMSLSLRSEDTAVYYCARSRDLLFPHYGMDVWGRTMT 120
Db 121 VSS 123
  |||
  121 VSS 123
QY 121 VSS 123
  |||
  121 VSS 123
Db 121 VSS 123

RESULT 9
US-10-293-418-2
; Sequence 2, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
```

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; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2

Query Match 100.0%; Score 640; DB 12; Length 249;
Best Local Similarity 100.0%; Pred. No. 8.8e-57;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  1 QVQLQSGAEVKKPGSSVRVSCASGCTFNNAIINWVROAPGQGLEWMGGIIPMFETAKY 60
  |||
  1 QVQLQSGAEVKKPGSSVRVSCASGCTFNNAIINWVROAPGQGLEWMGGIIPMFETAKY 60
Db 61 SQNFGRAVITADESTSTASMSLSLRSEDTAVYYCARSRDLLFPHYGMDVWGRTMT 120
  |||
  61 SQNFGRAVITADESTSTASMSLSLRSEDTAVYYCARSRDLLFPHYGMDVWGRTMT 120
QY 121 VSS 123
  |||
  121 VSS 123
Db 121 VSS 123

RESULT 10
US-10-293-418-471
; Sequence 471, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 471
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-471

Query Match 100.0%; Score 640; DB 12; Length 249;
Best Local Similarity 100.0%; Pred. No. 8.8e-57;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1  CURRENT FILING DATE: 2002-11-27
2  PRIOR APPLICATION NUMBER: 60/331,469
3  PRIOR FILING DATE: 2001-11-16
4  PRIOR APPLICATION NUMBER: 60/340,817
5  PRIOR FILING DATE: 2001-12-19
6  PRIOR APPLICATION NUMBER: 09/880,748
7  PRIOR FILING DATE: 2001-06-15
8  PRIOR APPLICATION NUMBER: 60/293,499
9  PRIOR FILING DATE: 2001-05-25
10 PRIOR APPLICATION NUMBER: 60/277,379
11 PRIOR FILING DATE: 2001-03-21
12 PRIOR APPLICATION NUMBER: 60/276,248
13 PRIOR FILING DATE: 2001-03-16
14 PRIOR APPLICATION NUMBER: 60/240,816
15 PRIOR FILING DATE: 2000-10-17
16 PRIOR APPLICATION NUMBER: 60/212,210
17 PRIOR FILING DATE: 2000-06-16
18 NUMBER OF SEQ ID NOS: 3247
19 SEQ ID NO 618
20 LENGTH: 249
21 TYPE: PRT
22 ORGANISM: Homo sapiens
23 US-10-293-418-618
24
25 Query Match 100.0%; Score 640; DB 12; Length 249;
26 Best Local Similarity 100.0%; Pred. NO. 8.8e-57;
27 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0
28
29 QY 1 QVQLQQSGAEVKKPKSSVRVSCCKASGTFNNNAINWVROAPGGGLEWGGIIIPFGTAKY 60
30 Db 1 QVQLQQSGAEVKKPKSSVRVSCCKASGTFNNNAINWVROAPGGGLEWGGIIIPFGTAKY 60
31
32 QY 61 SONFGRAVITADESTFASWELSLNSEDYAVYCARSDLLPFHYGMDVGRGTMT 120
33 Db 61 SONFGRAVITADESTFASWELSLNSEDYAVYCARSDLLPFHYGMDVGRGTMT 120
34
35 QY 121 VSS 123
36 Db 121 VSS 123
37
38 RESULT 13
39 US-10-293-418-719
40 Sequence 719, Application US/10293418
41 Publication No. US20030223996a1
42 GENERAL INFORMATION:
43 APPLICANT: Ruben et al.
44 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
45 FILE REFERENCE: PFS23P2
46 CURRENT APPLICATION NUMBER: US/10/293,418
47 CURRENT FILING DATE: 2002-11-27
48 PRIOR APPLICATION NUMBER: 60/331,469
49 PRIOR FILING DATE: 2001-11-16
50 PRIOR APPLICATION NUMBER: 60/340,817
51 PRIOR FILING DATE: 2001-12-19
52 PRIOR APPLICATION NUMBER: 09/880,748
53 PRIOR FILING DATE: 2001-06-15
54 PRIOR APPLICATION NUMBER: 60/293,499
55 PRIOR FILING DATE: 2001-05-25
56 PRIOR APPLICATION NUMBER: 60/277,379
57 PRIOR FILING DATE: 2001-03-21
58 PRIOR APPLICATION NUMBER: 60/276,248
59 PRIOR FILING DATE: 2001-03-16
60 PRIOR APPLICATION NUMBER: 60/240,816
61 PRIOR FILING DATE: 2000-10-17
62 PRIOR APPLICATION NUMBER: 60/212,210
63 PRIOR FILING DATE: 2000-06-16
64 NUMBER OF SEQ ID NOS: 3247
65 SEQ ID NO 719
66 LENGTH: 249
67 TYPE: PRT
68 ORGANISM: Homo sapiens
69 US-10-293-418-719

```

```
Query Match          100.0%; Score 640; DB 12; Length 249;
Best Local Similarity 100.0%; Pred. No. 8.8e-57;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGAEVKKPSSSVRVSCKASGTEFNNAIINWVROAPQGQLEMMGIIIPMGITAKY 60
   |||
Db 1 QVQLQSGAEVKKPSSSVRVSCKASGTEFNNAIINWVROAPQGQLEMMGIIIPMGITAKY 60

QY 61 SONFGQRAVITADESTSTASMEISLRSEDTAVYYCARSRDLLFPHYGMDVWGRTIWT 120
   |||
Db 61 SONFGQRAVITADESTSTASMEISLRSEDTAVYYCARSRDLLFPHYGMDVWGRTIWT 120

QY 121 VSS 123
   |||
Db 121 VSS 123

RESULT 14
Sequence 796, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 796
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
10-293-418-796

Query Match          100.0%; Score 640; DB 12; Length 249;
Best Local Similarity 100.0%; Pred. No. 8.8e-57;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGAEVKKPSSSVRVSCKASGTEFNNAIINWVROAPQGQLEMMGIIIPMGITAKY 60
   |||
Db 1 QVQLQSGAEVKKPSSSVRVSCKASGTEFNNAIINWVROAPQGQLEMMGIIIPMGITAKY 60

QY 61 SONFGQRAVITADESTSTASMEISLRSEDTAVYYCARSRDLLFPHYGMDVWGRTIWT 120
   |||
Db 61 SONFGQRAVITADESTSTASMEISLRSEDTAVYYCARSRDLLFPHYGMDVWGRTIWT 120

QY 121 VSS 123
   |||
Db 121 VSS 123

RESULT 15
US-09-880-748-1426
Sequence 1426, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1426
LENGTH: 246
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1426

Query Match          99.5%; Score 637; DB 10; Length 246;
Best Local Similarity 99.2%; Pred. No. 1.8e-56;
Matches 122; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGAEVKKPSSSVRVSCKASGTEFNNAIINWVROAPQGQLEMMGIIIPMGITAKY 60
   |||
Db 1 QVQLQSGAEVKKPSSSVRVSCKASGTEFNNAIINWVROAPQGQLEMMGIIIPMGITAKY 60

QY 61 SONFGQRAVITADESTSTASMEISLRSEDTAVYYCARSRDLLFPHYGMDVWGRTIWT 120
   |||
Db 61 SONFGQRAVITADESTSTASMEISLRSEDTAVYYCARSRDLLFPHYGMDVWGRTIWT 120

QY 121 VSS 123
   |||
Db 121 VSS 123
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Search completed: September 9, 2004, 11:23:42  
Job time: 91.4103 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 9, 2004, 10:59:50; Search time 13.6667 Seconds  
(without alignments)  
865.724 Million cell updates/sec

Title: US-09-880-748-2\_COPY\_1\_123  
Perfect score: 640  
Sequence: 1 QVQLQSGAEVKKPGSSSRV.....LFPHYGMDVGRGTWTVSS 123

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Minimum number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 70 summaries

Database : PIR 78:\*  
1: d1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	510	79.7	119	2	PH0961 Ig heavy chain V r
2	505.5	79.0	122	2	PH0958 Ig heavy chain V r
3	504.5	78.8	132	2	PH0954 Ig heavy chain V r
4	502	78.4	133	2	C33548 Ig heavy chain V-1
5	502	78.4	627	2	S14683 Ig mu chain precut
6	501.5	78.4	136	2	PH0960 Ig heavy chain V r
7	499.5	78.0	132	2	S46394 Ig heavy chain V r
8	498	77.8	127	2	PH0955 Ig heavy chain V r
9	494.5	77.3	126	2	B33548 Ig heavy chain V-1
10	491	76.7	135	2	PH0953 Ig heavy chain V-1
11	490	76.6	129	2	A33548 Ig heavy chain V-1
12	489.5	76.5	120	2	PH0962 Ig heavy chain V r
13	485.5	75.9	128	2	PH0952 Ig heavy chain V r
14	483.5	75.5	116	2	PH0959 Ig heavy chain V r
15	480	75.0	125	2	PH0957 Ig heavy chain V r
16	475	74.2	122	2	B49590 Ig heavy chain V r
17	468.5	73.2	116	2	S36261 Ig heavy chain V r
18	463.5	72.4	135	2	B32274 Ig heavy chain pre
19	452	70.6	113	2	PH1663 Ig heavy chain V r
20	450.5	70.4	108	2	PH1664 Ig heavy chain V r
21	445	69.5	123	2	S44108 Ig heavy chain V-D
22	444	69.4	98	2	S26915 Ig heavy chain V r
23	444	69.4	116	2	S31698 Ig heavy chain pre
24	440	68.8	98	2	S24680 Ig heavy chain V1
25	439	68.6	121	2	A49590 Ig heavy chain V r
26	435	68.0	119	2	S44106 Ig heavy chain V-D
27	429	66.7	117	1	G1H0EU Ig heavy chain V-1
28	427	66.7	109	2	PH1671 Ig heavy chain V r
29	425	66.4	109	2	PH1671 Ig heavy chain V r

## ALIGNMENTS

30	420.5	65.7	124	2	S19665 Ig heavy chain V r
31	419	65.5	129	2	S35260 Ig heavy chain V r
32	418	65.3	142	2	A32483 Ig heavy chain V r
33	416	65.0	98	2	A30523 Ig heavy chain V-1
34	416	65.0	98	2	S46463 Ig heavy chain V1
35	412.5	64.5	136	2	S31600 Ig heavy chain V r
36	411	64.2	116	2	S31667 Ig heavy chain V r
37	410.5	64.1	118	2	S32655 Ig heavy chain V r
38	408	63.7	97	2	PH0870 Ig heavy chain V r
39	404.5	63.2	119	2	F49590 Ig heavy chain V r
40	404.5	63.2	135	2	S49530 Ig heavy chain V r
41	400	62.5	123	2	D33548 Ig heavy chain V-1
42	397.5	62.1	118	2	PH1666 Ig heavy chain V r
43	397	62.0	127	2	S34014 Ig heavy chain V r
44	397	62.0	129	2	S46393 Ig heavy chain V r
45	394	61.6	160	2	PL0105 anti-PR2 erythrocy
46	391.5	61.2	114	2	PH1667 Ig heavy chain V r
47	390	60.9	121	2	S20783 Ig heavy chain V r
48	389	60.8	122	2	S36271 Ig heavy chain V r
49	388	60.6	148	2	S29257 Ig heavy chain V r
50	387.5	60.5	120	2	S31999 Ig heavy chain V r
51	387	60.5	131	2	S26792 Ig heavy chain V r
52	383.5	59.9	171	2	S23623 Ig heavy chain V r
53	382.5	59.8	104	2	PH1665 Ig heavy chain V r
54	379.5	59.3	143	1	E1H0ND Ig heavy chain pre
55	379	59.2	123	2	S20646 Ig heavy chain V r
56	379	59.2	142	2	S19245 Ig heavy chain pre
57	378.5	59.1	120	2	S26789 Ig heavy chain V r
58	377	58.9	138	2	E32513 Ig heavy chain pre
59	375.5	58.7	132	2	S31596 Ig heavy chain V r
60	374	58.4	117	1	HVH0HG Ig heavy chain pre
61	372.5	58.2	139	2	PS0024 Ig heavy chain pre
62	372.5	58.2	469	2	S37483 Ig gamma-2a chain
63	372	58.1	138	2	PH1565 Ig heavy chain V r
64	372	58.1	138	2	S21810 Ig heavy chain V r
65	371	58.0	125	2	S68170 Ig heavy chain V r
66	370.5	57.9	119	2	A24672 Ig heavy chain pre
67	369	57.7	144	2	E41287 Ig heavy chain pre
68	368	57.5	98	2	S25920 Ig heavy chain V r
69	368	57.5	134	2	S21916 Ig heavy chain V r
70	367.5	57.4	136	2	A49047 Ig heavy chain V r

## RESULT 1

Ig heavy chain V region (G6+ T-133) - human (fragment)  
PH0961  
C/Spectrum: Homo sapiens (man)  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
C/Accession: PH0961  
R/Martin, T.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A>Title: Evidence for somatic selection of natural autoantibodies.  
A/Reference number: PH0952; MVID:92202880; PMID:1552291  
A/Accession: PH0961  
A/Molecule type: DNA  
A/Status: nucleic acid sequence not shown  
A/Residues: 1-119 <MAR>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterodimer; immunoglobulin  
F/1-30/Region: framework 1  
F/15-98/Domain: immunoglobulin homology <IMM>  
F/31-35/Region: complementarity-determining 1  
F/36-50/Region: complementarity-determining 2  
F/51-67/Region: complementarity-determining 2  
F/68-98/Region: framework 3  
F/99-107/Region: complementarity-determining 3

## Query Match

Best Local Similarity 79.7%; Score 510; DB 2; Length 119;  
Matches 100; Conservative 9; Mismatches 10; Indels 4; Gaps 1;

QY 1 QVQLQSGAEVKKPSSSVKSCASGCTFNNNAIMWVROAPQGLEMMGGIIPMEGTAKY 60  
Db 1 QVQLVQSGAEVKKPSSSVKSCASGCTFSSVAISWVROAPQGLEMMGGIIPRGITANY 60  
QY 61 SONFGRAVLTADDESTSTASMSLSLRSEDTAVVYCARSDLLLPFHYGMDVWGRTWT 120  
Db 61 AOKFGRAVLTADDESTSTAYMELSLRSBEDTAVVYCARPNLPFA-VGMDVWGCTTWT 116  
QY 121 VSS 123  
Db 117 VSS 119

## RESULT 2

PH0958  
Ig heavy chain V region (G6+ CLT-HUR) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
Accession: PH0958  
Exp. Med. 175, 983-991, 1992  
A/Title: Evidence for somatic selection of natural autoantibodies.  
A/Reference number: PH0952; PMID:92202880; PMID:1552291  
A/Accession: PH0958  
A/Status: nucleic acid sequence not shown  
A/Molecule type: DNA  
A/Residues: 1-122 <MAR>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F.15-98/Region: framework 1  
F.15-98/Domain: immunoglobulin homology <IMM>  
F.31-35/Region: complementarity-determining 1  
F.36-50/Region: framework 2  
F.51-67/Region: complementarity-determining 2  
F.68-98/Region: framework 3  
F.99-110/Region: complementarity-determining 3

Query Match 79.0%; Score 505.5; DB 2; Length 122;  
Best Local Similarity 82.1%; Pred. No. 8.4e-40;  
Matches 101; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

QY 1 QVQLQSGAEVKKPSSSVKSCASGCTFNNNAIMWVROAPQGLEMMGGIIPMEGTAKY 60  
Db 1 QVQLVQSGAEVKKPSSSVKSCASGCTFSSVAISWVROAPQGLEMMGGIIPRGITANY 60  
QY 61 SONFGRAVLTADDESTSTASMSLSLRSEDTAVVYCARSDLLLPFHYGMDVWGRTWT 120  
Db 61 AOKFGRAVLTADDESTSTAYMELSLRSBEDTAVVYCARPNLPFA-VGMDVWGCTTWT 119  
QY 121 VSS 123  
Db 120 VSS 122

## RESULT 3

PH0954  
Ig heavy chain V region (G6+ CLT-HEN) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
Accession: PH0954  
Exp. Med. 175, 983-991, 1992  
A/Title: Evidence for somatic selection of natural autoantibodies.  
A/Reference number: PH0952; PMID:92202880; PMID:1552291  
A/Accession: PH0954  
A/Status: nucleic acid sequence not shown  
A/Molecule type: DNA  
A/Residues: 1-112 <MAR>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F.15-98/Domain: immunoglobulin homology <IMM>

F.31-35/Region: complementarity-determining 1  
F.36-50/Region: framework 2  
F.51-67/Region: complementarity-determining 2  
F.68-98/Region: framework 3  
F.99-120/Region: complementarity-determining 3

Query Match 78.8%; Score 504.5; DB 2; Length 132;  
Best Local Similarity 76.5%; Pred. No. 1.1e-39;  
Matches 101; Conservative 10; Mismatches 12; Indels 9; Gaps 2;

QY 1 QVQLQSGAEVKKPSSSVKSCASGCTFNNNAIMWVROAPQGLEMMGGIIPMEGTAKY 60  
Db 1 QVQLVQSGAEVKKPSSSVKSCASGCTFSSVAISWVROAPQGLEMMGGIIPRGITANY 60  
QY 61 SONFGRAVLTADDESTSTASMSLSLRSEDTAVVYCARSDLLLPFHYGMDVWGRTWT 111  
Db 61 AOKFGRAVLTADDESTSTAYMELSLRSBEDTAVVYCARPHASIDDPWGSQYENNYGMD 120  
QY 112 VWGRTWTVSS 123  
Db 121 VWGCTTWTVSS 132

## RESULT 4

C33548  
Ig heavy chain V-1 region (783) - human  
C/Species: Homo sapiens (man)  
C/Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996  
Accession: C33548  
R/Kips, T.D.; Tomhave, E.; Pratt, L.F.; Duffly, S.; Chen, P.P.; Carson, D.A.  
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989  
A/Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr  
A/Reference number: A33548; PMID:8934575; PMID:2503826  
A/Accession: C33548  
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A/Molecule type: DNA  
A/Residues: 1-133 <KIP>  
A/Experimental source: the sequence was determined from the differentiated gene  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F.15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 502; DB 2; Length 133;  
Best Local Similarity 74.8%; Pred. No. 1.9e-39;  
Matches 101; Conservative 11; Mismatches 9; Indels 14; Gaps 2;

QY 1 QVQLQSGAEVKKPSSSVKSCASGCTFNNNAIMWVROAPQGLEMMGGIIPMEGTAKY 60  
Db 1 QVQLVQSGAEVKKPSSSVKSCASGCTFSSVAISWVROAPQGLEMMGGIIPRGITANY 60  
QY 61 SONFGRAVLTADDESTSTASMSLSLRSEDTAVVYCARSDLLLPFHYGMDVWGRTWT 108  
Db 61 AOKFGRAVLTADDESTSTAYMELSLRSBEDTAVVYCARPTG--ILGYSGWYPSNDYXX 118  
QY 109 GMDVWGRTWTVSS 123  
Db 119 GMDVWGCTTWTVSS 133

## RESULT 5

S14683  
Ig mu chain precursor, membrane-bound (clone 201) - human  
C/Species: Homo sapiens (man)  
C/Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 23-Jul-1999  
Accession: S14683; S08047  
R/Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.  
Nucleic Acids Res. 18, 4278, 1990  
A/Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain  
A/Reference number: S14683; PMID:90332450; PMID:2115996  
A/Accession: S14683  
A/Molecule type: mRNA  
A/Residues: 1-627 <FRI>  
A/Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451

C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin; membrane protein  
F:1-15/Domain: signal sequence #status predicted <SIG-  
F:16-627/Product: 19 mu chain #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 502; DB 2; Length 627;  
Best Local Similarity 74.8%; Pred. No. 1e-38;  
Matches 101; Conservative 11; Mismatches 9; Indels 14; Gaps 2;

QY 1 QVQLQSGAEVKKPGSSSVASCASGCTFNNAIINVRQAPQGLEWMGIIIPMFGTAY 60  
DB 20 QVQLVQSGAEVKKPGSSSVASCASGCTFSSVAISVWRQAPQGLEWMGIIIPFGTANY 79  
QY 61 SQNPGQRAVITADESTSTASMLSLRSRSDTAIVYCARSDLLLPF-----HY 108  
DB 80 AAKFGQRTVITADESTSTASMLSLRSRSDTAIVYCAKRGK--ILGYSYSGWYPNSDYY 137  
QY 109 GMDVNGRGTMTVSS 123  
DB 138 GMDVNGGCTTVTVSS 152

## RESULT 6

PH0960  
Ig heavy chain V region (G6+ T-130) - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996

C:Accession: PH0960

R:Martin, T.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A:Title: Evidence for somatic selection of natural autoantibodies.  
A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0960

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-50/Region: framework 2

F:51-67/Region: complementarity-determining 2

F:68-98/Region: framework 3

F:99-124/Region: complementarity-determining 3

Query Match 78.4%; Score 501.5; DB 2; Length 136;  
Best Local Similarity 73.5%; Pred. No. 2.2e-39;  
Matches 100; Conservative 10; Mismatches 13; Indels 13; Gaps 1;

QY 1 QVQLQSGAEVKKPGSSSVASCASGCTFNNAIINVRQAPQGLEWMGIIIPMFGTAY 60  
DB 1 QVQLVQSGAEVKKPGSSSVASCASGCTFSSVAISVWRQAPQGLEWMGIIIPFGTANY 60  
QY 61 SQNPGQRAVITADESTSTASMLSLRSRSDTAIVYCARSDLLP-----LFP 107  
DB 61 AAKFGQRTVITADESTSTASMLSLRSRSDTAIVYCARSTRVSTLYDSSGYYDFSG 120  
QY 108 YGMDVNGRGTMTVSS 123  
DB 121 YGMDVNGGCTTVTVSS 136

## RESULT 7

S46394  
Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000

C:Accession: S46394

R:Figini, M.; Marke, J.D.; Winter, G.; Griffiths, A.D.

J. Mol. Biol. 239, 68-78, 1994

A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by

A:Reference number: S46390; MUID:94254092; PMID:8196048

A:Accession: S46394

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-132 <PIG>

A:Cross-references: EMBL:231681; NID:G509788; PIDN:CAA83486.1; PID:G1335147

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 499.5; DB 2; Length 132;  
Best Local Similarity 75.8%; Pred. No. 3.3e-39;  
Matches 100; Conservative 12; Mismatches 11; Indels 9; Gaps 1;

QY 1 QVQLQSGAEVKKPGSSSVASCASGCTFNNAIINVRQAPQGLEWMGIIIPMFGTAY 60  
DB 1 QVQLVQSGAEVKKPGSSSVASCASGCTFSSVAISVWRQAPQGLEWMGIIIPFGTANY 60  
QY 61 SQNPGQRAVITADESTSTASMLSLRSRSDTAIVYCARSR-----DLLLPHYGMD 111  
DB 61 AAKFGQRTVITADESTSTASMLSLRSRSDTAIVYCARQLPADTGILEWLPSTYYMD 120  
QY 112 YMGRTMTVSS 123  
DB 121 YMGKGTMTVSS 132

## RESULT 8

PH0955

Ig heavy chain V region (G6+ CTL-AND) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996

C:Accession: PH0955

R:Martin, T.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A:Title: Evidence for somatic selection of natural autoantibodies.  
A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0955

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-50/Region: framework 2

F:51-67/Region: complementarity-determining 2

F:68-98/Region: framework 3

F:99-115/Region: complementarity-determining 3

Query Match 77.8%; Score 498; DB 2; Length 127;  
Best Local Similarity 78.7%; Pred. No. 4.3e-39;  
Matches 100; Conservative 8; Mismatches 15; Indels 4; Gaps 1;

QY 1 QVQLQSGAEVKKPGSSSVASCASGCTFNNAIINVRQAPQGLEWMGIIIPMFGTAY 60  
DB 1 QVQLVQSGAEVKKPGSSSVASCASGCTFSSVAISVWRQAPQGLEWMGIIIPFGTANY 60  
QY 61 SQNPGQRAVITADESTSTASMLSLRSRSDTAIVYCARSDLLLP-----YGMVNGRG 116  
DB 61 AAKFGQRTVITADESTSTASMLSLRSRSDTAIVYCARISIGVQHYYYYYYMDVWGKG 120  
QY 117 TMTVSS 123  
DB 121 TTVTVSS 127

## RESULT 9

B35348

Ig heavy chain V-1 region (AND) - human

C:Species: Homo sapiens (man)

C:Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996

C:Accession: B33548  
R:Kipps, T.V.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.  
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989  
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr  
A:Reference number: A33548; MUID:89345575; PMID:2503826  
A:Accession: B33548  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: DNA  
A:Residues: 1-126 <KIP>  
A:Experimental source: the sequence was determined from the differentiated gene  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.3%; Score 494.5; DB 2; Length 126;  
Best Local Similarity 79.4%; Pred. No. 9e-39;  
Matches 100; Conservative 7; Mismatches 16; Indels 3; Gaps 1;

QY 1 QVQLQSGAEVKKPSSSVKSCASGCTFNNAIMNWROAPQGLEMMGGIIPMEGTAKY 60  
1 QVQLVQSGAEVKKPSSSVKSCASGCTFSYALISWROAPQGLEMMGGIIPRGITANY 60  
QY 61 SQNFGQVAITADESTSTASMLSLRSRSDTAIVYYCARSDLLFPFH--YGDVWGRGT 117  
61 AAKFGQGVITTADESTSTAYMELSLRSRSDTAIVYYCARVSIQVQHYVYVMDVWGLGT 120  
DB 61 AAKFGQGVITTADESTSTAYMELSLRSRSDTAIVYYCARVSIQVQHYVYVMDVWGLGT 120  
QY 118 MVTVSS 123  
121 TVTVSS 126  
DB 121 TVTVSS 126

## RESULT 10

PH0953  
Ig heavy chain V region (G6+ CL1-SIC) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
C:Accession: PH0953  
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A:Title: Evidence for somatic selection of natural autoantibodies.  
A:Reference number: PH0952; MUID:92202880; PMID:1552291  
A:Accession: PH0953  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-135 <MAR>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-30/Region: framework 1  
F:1-30/Domain: immunoglobulin homology <IMM>  
F:36-50/Region: complementarity-determining 1  
F:51-67/Region: complementarity-determining 2  
F:68-98/Region: framework 3  
F:99-123/Region: complementarity-determining 3

Query Match 76.7%; Score 491; DB 2; Length 135;  
Best Local Similarity 75.6%; Pred. No. 2e-38; Indels 12; Gaps 2;  
Matches 102; Conservative 7; Mismatches 14;

QY 1 QVQLQSGAEVKKPSSSVKSCASGCTFNNAIMNWROAPQGLEMMGGIIPMEGTAKY 60  
1 QVQLVQSGAEVKKPSSSVKSCASGCTFSYALISWROAPQGLEMMGGIIPRGITANY 60  
QY 61 SQNFGQVAITADESTSTASMLSLRSRSDTAIVYYCAR-----SRDLL---PPHY 108  
61 AAKFGQGVITTADESTSTAYMELSLRSRSDTAIVYYCARNGYCGDGYRHWELLRFDFSED 120  
DB 61 AAKFGQGVITTADESTSTAYMELSLRSRSDTAIVYYCARNGYCGDGYRHWELLRFDFSED 120  
QY 109 GMDVWGRGTMTVSS 123  
121 AFDVWGRGTMTVSS 135  
DB 121 AFDVWGRGTMTVSS 135

## RESULT 11

A33548  
Ig heavy chain V-1 region (NEI) - human  
C:Species: Homo sapiens (man)  
C:Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996  
C:Accession: A33548; PH0956  
R:Kipps, T.V.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.  
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989  
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr  
A:Reference number: A33548; MUID:89345575; PMID:2503826  
A:Accession: A33548  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-129 <KIP>  
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A:Title: Evidence for somatic selection of natural autoantibodies.  
A:Reference number: PH0952; MUID:92202880; PMID:1552291  
A:Accession: PH0956  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-129 <MAR>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-30/Region: framework 1  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1  
F:36-50/Region: complementarity-determining 2  
F:51-67/Region: complementarity-determining 2  
F:68-98/Region: framework 3  
F:99-117/Region: complementarity-determining 3

Query Match 76.6%; Score 480; DB 2; Length 129;  
Best Local Similarity 76.3%; Pred. No. 2.4e-38;  
Matches 100; Conservative 11; Mismatches 10; Indels 10; Gaps 3;

QY 1 QVQLQSGAEVKKPSSSVKSCASGCTFNNAIMNWROAPQGLEMMGGIIPMEGTAKY 60  
1 QVQLVQSGAEVKKPSSSVKSCASGCTFSYALISWROAPQGLEMMGGIIPRGITANY 60  
DB 1 QVQLVQSGAEVKKPSSSVKSCASGCTFSYALISWROAPQGLEMMGGIIPRGITANY 60  
QY 61 SQNFGQVAITADESTSTASMLSLRSRSDTAIVYYCARSDLLFPFH--YGDVWGRGT 117  
61 AAKFGQGVITTADESTSTAYMELSLRSRSDTAIVYYCARVSIQVQHYVYVMDVWGLGT 120  
DB 61 AAKFGQGVITTADESTSTAYMELSLRSRSDTAIVYYCARVSIQVQHYVYVMDVWGLGT 120  
QY 113 MGRGTMTVSS 123  
121 MGRGTMTVSS 129  
DB 121 MGRGTMTVSS 129

## RESULT 12

PH0962  
Ig heavy chain V region (G6+ T-142) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
C:Accession: PH0962  
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A:Title: Evidence for somatic selection of natural autoantibodies.  
A:Reference number: PH0952; MUID:92202880; PMID:1552291  
A:Accession: PH0962  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-120 <MAR>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-30/Region: framework 1  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1  
F:36-50/Region: complementarity-determining 2  
F:51-67/Region: complementarity-determining 2  
F:68-98/Region: framework 3  
F:99-108/Region: complementarity-determining 3

Query Match 76.5%; Score 489.5; DB 2; Length 120;



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 9, 2004, 10:58:34 : Search time 8.9359 Seconds

(without alignments)  
716.730 Million cell updates/sec

Title: US-09-880-748-2\_COPY\_1\_123

Perfect score: 640  
Sequence: 1 QVQLQSGAEVKKPKSSSVRV.....LRFHYGMDVGRGTWTYSS 123

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 70 summaries

Database : SwissProt\_42.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	427	66.7	117	1	HV1A_HUMAN
2	379.5	59.3	147	1	HV1C_HUMAN
3	374	58.4	117	1	HV1B_HUMAN
4	359	56.1	120	1	HV03_MOUSE
5	356	55.6	140	1	HV02_MOUSE
6	353.5	55.2	139	1	HV07_MOUSE
7	350	54.7	117	1	HV13_MOUSE
8	349	54.5	117	1	HV1G_HUMAN
9	347	54.2	117	1	HV12_MOUSE
10	345.5	54.0	114	1	HV00_MOUSE
11	344.5	53.8	118	1	HV01_MOUSE
12	341	53.3	121	1	HV01_MOUSE
13	341	53.3	138	1	HV48_MOUSE
14	338.5	52.9	120	1	HV1H_HUMAN
15	338.5	52.9	137	1	HV11_MOUSE
16	330.5	51.6	120	1	HV50_MOUSE
17	329	51.4	125	1	HV1F_HUMAN
18	328.5	51.3	124	1	HV1D_HUMAN
19	328	51.2	117	1	HV52_MOUSE
20	318.5	49.8	124	1	HV1E_HUMAN
21	314	49.1	117	1	HV05_HUMAN
22	313	48.9	136	1	HV15_MOUSE
23	311	48.6	117	1	HV06_MOUSE
24	309	48.3	121	1	HV3J_HUMAN
25	308	48.1	117	1	HV04_MOUSE
26	308	48.1	117	1	HV09_MOUSE
27	307.5	48.0	122	1	HV3G_HUMAN
28	305	47.7	119	1	HV3I_HUMAN
29	303	47.3	117	1	HV43_MOUSE
30	301	46.9	117	1	HV14_MOUSE
31	300	46.9	117	1	HV10_MOUSE
32	299.5	46.8	136	1	HV16_MOUSE
33	295.5	46.2	114	1	HV3B_HUMAN

## ALIGNMENTS

34	295	46.1	115	1	HV3D_HUMAN	P01765 homo sapien
35	292.5	45.7	122	1	HV3H_HUMAN	P01769 homo sapien
36	291	45.5	117	1	HV42_MOUSE	P01812 mus musculu
37	287.5	44.9	119	1	HV38_MOUSE	P01808 mus musculu
38	284.5	44.5	146	1	HV21_HUMAN	P06331 homo sapien
39	281.5	44.0	119	1	HV40_MOUSE	P01810 mus musculu
40	280	43.8	123	1	HV22_MOUSE	P01791 mus musculu
41	279.5	43.7	116	1	HV3T_HUMAN	P01781 homo sapien
42	278	43.4	117	1	HV02_CANFA	P01781 homo sapien
43	277.5	43.4	126	1	HV3K_HUMAN	P01772 homo sapien
44	276.5	43.2	119	1	HV37_MOUSE	P01807 mus musculu
45	275.5	43.0	122	1	HV3A_HUMAN	P01762 homo sapien
46	275	43.0	115	1	HV3P_HUMAN	P01767 homo sapien
47	275	43.0	120	1	HV3E_HUMAN	P01766 mus musculu
48	273	42.7	117	1	HV41_MOUSE	P01811 mus musculu
49	270.5	42.3	119	1	HV3P_HUMAN	P01777 homo sapien
50	267.5	41.8	120	1	HV3U_HUMAN	P01782 homo sapien
51	266	41.6	116	1	HV3R_HUMAN	P01779 homo sapien
52	266	41.6	117	1	HV3C_HUMAN	P01764 homo sapien
53	264.5	41.3	122	1	HV21_MOUSE	P01790 mus musculu
54	264	41.2	117	1	HV2G_HUMAN	P01784 mus musculu
55	264	41.2	142	1	HV01_RAT	P01805 mus musculu
56	263.5	41.2	118	1	HV3V_HUMAN	P01805 mus musculu
57	263.5	41.2	122	1	HV20_MOUSE	P01789 mus musculu
58	263	41.1	123	1	HV18_MOUSE	P01787 mus musculu
59	263	41.1	123	1	HV19_MOUSE	P01788 mus musculu
60	262	40.9	123	1	HV25_MOUSE	P01794 mus musculu
61	261	40.8	113	1	HV30_MOUSE	P01799 mus musculu
62	261	40.8	115	1	HV32_MOUSE	P01801 mus musculu
63	261	40.8	123	1	HV23_MOUSE	P01802 mus musculu
64	259.5	40.5	114	1	HV01_CANFA	P01784 canis fam11
65	259	40.5	118	1	HV39_MOUSE	P01809 mus musculu
66	259	40.5	129	1	HV2F_HUMAN	P01824 homo sapien
67	258	40.3	116	1	HV3Q_HUMAN	P01778 homo sapien
68	258	40.3	119	1	HV3L_HUMAN	P01773 homo sapien
69	257.5	40.2	111	1	HV35_MOUSE	P01804 mus musculu
70	257.5	40.2	115	1	HV3S_HUMAN	P01780 homo sapien

RESULT 1  
HV1A\_HUMAN STANDARD; PRT; 117 AA.  
ID HV1A\_HUMAN  
AC P01742;  
DT 21-JUL-1986 (rel. 01, Created)  
DT 21-JUL-1986 (rel. 01, Last sequence update)  
DT 10-OCT-2003 (rel. 42, Last annotation update)  
DE Ig heavy chain V-I region EU.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP MEDLINE=71064024; PubMed=5489771;  
RX Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
RA Waxdal M.J., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino  
acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";  
RL Biochemistry 9:3161-3170(1970).  
RN [2]  
RP DISULFIDE BOND.  
RX MEDLINE=71064027; PubMed=4923144;  
RA Gall W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X.  
Intrachain disulfide bonds.";  
RL Biochemistry 9:3188-3196(1970).  
CC -I- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS  
MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A90563; GIHUEU.

```

DR HSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Pyroliidone carboxylic acid.
KW MOD RES 1 112
FT MOD RES 1 112
FT DISTLFD 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12472 MW; 99D60ADAEED52818 CRC64;

Query Match
Best Local Similarity 66.7%; Score 427; DB 1; Length 117;
Matches 87; Conservative 9; Mismatches 21; Indels 6; Gaps 1;

1 QVQLQSGAEVKKPGSSVRVSCKASGCTFNNAINWVROAPQGLEWMGIIIPMGCTAKY 60
1 QVQLVQSGAEVKKPGSSVRVSCKASGCTFSRAIIWVROAPQGLEWMGIIIPMGCPY 60
1 SQNPGRAVITADESTSMELSLRSDTAIVYCARSDLLFPHYGMDVWGCTMYT 120
61 AKPFGRVITADESTSMELSLRSDTAIVYCARSDLLFPHYGMDVWGCTMYT 114
61 AAKPFGRVITADESTSMELSLRSDTAIVYCARSDLLFPHYGMDVWGCTMYT 114
121 VSS 123
115 VSS 117

RESULT 2
HVIC HUMAN STANDARD; PRT; 147 AA.
ID HVIC_HUMAN
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OC NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=83065234; PubMed=6815656;
Kenan J.H., Molgaard H.V., Houghton M., Derlyshire R.B., Viney J.,
Bell L.O., Gould H.U.;
"Cloning and sequence determination of the gene for the human
immunoglobulin epsilon chain expressed in a myeloma cell line.";
Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
[2]
SEQUENCE OF 20-147.
RA Benrich H.H., Johanson S.G.O., von Bahr-Lindstrom H.;
(in) Bach M.K. (eds.);
Immediate hypersensitivity: modern concepts and developments, pp.1-36,
Marcel Dekker, New York (1978).
-1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
PROTEIN.
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
HSP; P01789; IMCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; Pyroliidone carboxylic acid.
FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.

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FT DOMAIN 20 131
FT MOD RES 20 20
FT DISTLFD 41 115
FT CONFLICT 21 21
FT CONFLICT 53 54
FT CONFLICT 67 68
FT CONFLICT 125 125
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match
Best Local Similarity 59.3%; Score 379.5; DB 1; Length 147;
Matches 78; Conservative 17; Mismatches 28; Indels 5; Gaps 2;

1 QVQLQSGAEVKKPGSSVRVSCKASGCTFNNAINWVROAPQGLEWMGIIIPMGCTAKY 60
20 QVQLVQSGAEVKKPGSSVRVSCKASGCTFNNAINWVROAPQGLEWMGIIIPMGCTAKY 79
61 SQNPGRAVITADESTSMELSLRSDTAIVYCARSDLLFPHYGMDVWGCTMYT 115
80 AKPFGRVITADESTSMELSLRSDTAIVYCARSDLLFPHYGMDVWGCTMYT 139
116 GTTVTVSS 123
140 GTTVTVSS 147

RESULT 3
HVIC HUMAN STANDARD; PRT; 117 AA.
ID HVIC_HUMAN
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region Hg3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OC NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=83144028; PubMed=6298778;
Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
(VH) gene subgroups.";
Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
-1- SWISS-PROT entry is copyright. It is produced through a collaboration
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-----
CC EMBL; J00240; AAAS2968.1; -.
DR PIR; A02024; HVH0HG.
DR HSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
FT DOMAIN 20 117 IG-LIKE.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

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[illegible]

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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DS Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152816; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estes P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RL immunoglobulin heavy chain."
RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC or send an email to license@isb-eb.ch).
CC -----
CC EMBL; J00493; AAA38128.1; -.
DR PIR; A94264; HVMSG7.
DR HSSP; P01810; 2PBJ..
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; Ig_LIKE; 1.
DR Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query March 55.6%; Score 356; DB 1; Length 140;
Best Local Similarity 55.9%; Pred. No. 3,56-30;
Matches 71; Conservative 21; Mismatches 25; Indels 10; Gaps 2;

QY 1 QVQLQSGAEVKKPKSSVRVSCAKSGTTPNNAINWVQAPQGLEWMGGIPEFGTAKY 60
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 20 EVQLQSGAEIVRAGSSVVKMSCKASGTFISYGINWVKORPQGLEWIGYINPENGYN 79
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 61 SQNRQGRVAITADSTSTASHELSLSRSEPTAVYYCARSDLLFFHYG---MDVWG 116
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 80 NEKRGKQITTLVDKSSSTAYQMLRSLTSEDSAVYFCARSH-----YYGSDYDP 133
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 117 TMWTVSS 123
   |::|::|
DB 134 TPLTVSS 140

RESULT 6
HV07 MOUSE
ID _HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region BI-8/186-2 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;

```

RA Bothwell A.L.M., Paskind M., Rath M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the NPB family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
 RL Cell 24:625-637(1981).  
 CC -1- MISCELLANEOUS: THE BI-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA  
 CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL  
 CC (NPB ANTIBODIES).  
 CC -----  
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 CC -----  
 CC EMBL: J00529; AAA38170.1; -.  
 DR PIR: A90809; MEMS18.  
 DR PDB: 1A6U; 27-MAY-98.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF00047; IG\_1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG-LIKE; 1.  
 DR Immunoglobulin V region; Signal; 3D-structure.  
 DR SIGNAL 1 19  
 FT CHAIN 1 19 IG HEAVY CHAIN V REGION BI-8/186-2.  
 FT DOMAIN 20 139 FRAMEWORK-1.  
 FT DOMAIN 20 49 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 50 54 FRAMEWORK-2.  
 FT DOMAIN 55 68 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 69 85 FRAMEWORK-3.  
 FT DOMAIN 86 117 D SEGMENT.  
 FT DOMAIN 118 124 JH2 SEGMENT.  
 FT DOMAIN 125 139 BY SIMILARITY.  
 FT DISULFID 41 115  
 FT NON\_TER 139 139  
 SQ SEQUENCE 139 AA; 15419 MW; 1B57DDAFDC9F465 CRC64;  
 Query Match 55.2%; Score 353.5; DB 1; Length 139;  
 Best Local Similarity 54.8%; Pred. No. 6.3e-30;  
 Matches 69; Conservative 23; Mismatches 25; Indels 9; Gaps 2;  
 QY 1 QVQLQSGAEVKKPGSSVRVSCKASGCTFNNNAIMVWQAPGQGLEWMGIIIMFGTANY 60  
 Db 20 QVQLQSPGAEIVKPGASVSKSCASGYTFSTYMMHWKQPRGLRWIGRIDPNSGGTXY 79  
 Db 61 SONFGQVAITADESTSTASMEISLRSEDTAVYYCARSDLLLPHYG--MDVWGRT 117  
 Db 80 NEFKSKATLTVDKPSSTAYMQLSTSEDSAVYYCAR-----YDIYSSYFDYWGQGT 133  
 QY 118 MVTVSS 123  
 Db 134 TLTVSS 139  
 RESULT 7  
 ID HV13 MOUSE STANDARD; PRT; 117 AA.  
 AC P01757;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 02, Last annotation update)  
 DE Ig heavy chain V region J558.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RX MEDLINE=80078170; PubMed=6765983;  
 RA Schilling J., Clevinger B., Davie J.M., Hood L.;

RT "Amino acid sequence of homogeneous antibodies to dextran and DNA  
 RT rearrangements in heavy chain V-region gene segments.";  
 RL Nature 283:35-40(1980).  
 CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO  
 CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF  
 CC WHICH OCCUR IN THE D AND J SEGMENTS.  
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR: A26242; MEMS15.  
 DR HSSP: P01789; IMCP.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF00047; IG\_1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG-LIKE; 1.  
 DR Immunoglobulin V region.  
 DR DOMAIN 1 116 IG-LIKE.  
 FT DISULFID 22 96 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE47E41 CRC64;  
 Query Match 54.7%; Score 350; DB 1; Length 117;  
 Best Local Similarity 55.3%; Pred. No. 1.2e-29;  
 Matches 68; Conservative 22; Mismatches 27; Indels 6; Gaps 1;  
 QY 1 QVQLQSGAEVKKPGSSVRVSCKASGCTFNNNAIMVWQAPGQGLEWMGIIIMFGTANY 60  
 Db 1 EVQLQSPGAEIVKPGASVSKSCASGYTFDTYMMHWKQPRGLRWIGRIDPNNGGTXY 60  
 QY 61 SONFGQVAITADESTSTASMEISLRSEDTAVYYCARSDLLLPHYGMDVWGRT 120  
 Db 61 NQFKSKATLTVDKPSSTAYMQLSTSEDSAVYYCAR-----YWFYDWGAGTIVT 114  
 QY 121 VSS 123  
 Db 115 VSS 117  
 RESULT 8  
 ID HV1G HUMAN STANDARD; PRT; 117 AA.  
 AC P23083;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-1 region V35 precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RX MEDLINE=88296408; PubMed=2841108;  
 RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.O.,  
 RA Ohno H., Fukuhara S., Honjo T.;  
 RT "Dispersed localization of D segments in the human immunoglobulin  
 RT heavy-chain locus.";  
 RL EMBO J. 7:1047-1051(1988).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
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 CC -----  
 CC EMBL: X07448; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: S00476; HVH035.  
 DR HSSP: P01772; 2PB4.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding; NAS.

[illegible]

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Db      1 10KFKGKATLTVYDSSSTAYWQANLSUTSEDSAYVYCAADYD-----WYFDWKGAGTIVT 114
Qy      121 VSS 123
        |||
Db      115 VSS 117

RESULT 10
HV00_MOUSE STANDARD; PRT; 114 AA.
ID HV00_MOUSE
AC P01741;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region (Anti-arsenate antibody).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=79195438; PubMed=109536;
RA Capra J.D., Nisenson A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. VII. The complete amino acid sequence of the heavy
RT chain variable region of anti-P-azophenylarsenate antibodies from A/J
RT mice bearing a cross-reactive idiotype.";
RL J. Immunol. 123:279-284(1979).
-1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
THE IGH1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
REGION SEQUENCE.
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC CC
CC PIR: A02022; GIMSA4.
DR HSSP: P01772; 2PBA.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SMO0406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR IMMUNOGLOBULIN V region.
KW DOMAIN
FT NON TER 114 IG-LIKE.
FT 106
SQ SEQUENCE 114 AA; 12555 MM; 99DDBF086A69F4BE CRC64;

Query Match 54.0%; Score 345.5; DB 1; Length 114;
Best local similarity 61.3%; Pred. No. 3.4e-29;
Matches 73; Conservative 16; Mismatches 25; Indels 5; Gaps 2.

Qy      1 QVQLQSGAEVKKPKGSSSVKSCAKSGGTFNNNAINWYQAPGQGLEWMGIIIPMEGTANY 60
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      1 EVQLQSGAEIVKAGSSVKMSCKATGTFSSYELWYRQAGQGLEDDGYISSSAYINY 60
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy      61 SQNFGRAVITADESTSTASNELSLRSEDTAVYYCARSDLLFPHYGMDVWGRTNV 119
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 AQKFGRAVITADESTTAYWELSLRSEDTAVYFCA---VRVYSRY-FDGMGQGLTV 114
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 11
HV51_MOUSE STANDARD; PRT; 118 AA.
ID HV51_MOUSE
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.

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Db 135 TFS 138

## RESULT 14

RT HVL1\_HUMAN STANDARD; PRT; 120 AA.  
 AC P80421;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-1 region DOT.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE.  
 RT MEDLINE=9525298; PubMed=7737190;  
 RT Stoppini M., Bellocchi V., Negri A., Merlini G., Garver F., Ferri G.;  
 RT "Characterization of the two unique human anti-flavin monoclonal  
 RT immunoglobulins";  
 RT Eur. J. Biochem. 228:886-893(1995).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR HSP; P01772; 2F84.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; P:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_V.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR Immunoglobulin V region.  
 FT DOMAIN 1 111 IG-LIKE.  
 FT DISULFID 22 95 BY SIMILARITY.  
 FT NON TER 120 120  
 SQ SEQUENCE 120 AA; 13272 MW; F1307FD253A782F1 CRC64;  
 Query Match 52.9%; Score 338.5; DB 1; Length 120;  
 Best Local Similarity 58.5%; Pred. No. 2e-28;  
 Matches 72; Conservative 16; Mismatches 30; Indels 5; Gaps 3;  
 QY 2 VOLQSGAEVKKPGSSVRVSCKASGTFNNNAIMVWROAPGQGLMMGGIIPMGTAKS 61  
 DB 2 VOLQSGAEVKKPGSSVRVSCKASGTFNNNAIMVWROAPGQGLMMGGIIPMGTAKS 61  
 DB 62 QNFQGVATTADESTSTASMEISLRSEDTAVYYCAR-SRDLLPFGYGMVWGKGTMT 120  
 DB 61 EKFRDLVWSSDTSANTVMQLNLRSDDTGRYFCARVSD--FQYGMVWGKGTMT 117  
 QY 121 VSS 123  
 DB 118 VSS 120  
 RESULT 15  
 RT HVL1\_MOUSE STANDARD; PRT; 137 AA.  
 AC P01755;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region S43 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81234548; PubMed=6788376;  
 RA Bothwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;

RT "Heavy chain variable region contribution to the NPB family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
 RT Cell 24:625-637(1981).  
 CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN mRNA WAS CLONED FROM A HYBRIDOMA  
 CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL  
 CC (NPB ANTIBODIES).  
 CC (NPB ANTIBODIES).  
 CC -----  
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 CC -----  
 CC EMBL; J00539; AAA8172.1; -.  
 DR PIR; A02038; GZMS43.  
 DR HSP; P01810; 2F8J.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.  
 FT DOMAIN 20 49 FRAMEWORK-1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 86 117 FRAMEWORK-3.  
 FT DOMAIN 118 122 D SEGMENT.  
 FT DOMAIN 123 137 JH2 SEGMENT.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON TER 137 137  
 SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF448BEC9 CRC64;

Query Match 52.9%; Score 338.5; DB 1; Length 137;  
 Best Local Similarity 55.3%; Pred. No. 2.3e-28;  
 Matches 68; Conservative 20; Mismatches 30; Indels 5; Gaps 2;  
 QY 1 QVOLQSGAEVKKPGSSVRVSCKASGTFNNNAIMVWROAPGQGLMMGGIIPMGTAKY 60  
 DB 20 QVOLQSGAEVKKPGSSVRVSCKASGTFNNNAIMVWROAPGQGLMMGGIIPMGTAKY 79  
 QY 61 SONFQGVATTADESTSTASMEISLRSEDTAVYYCAR-SRDLLPFGYGMVWGKGTMT 120  
 DB 80 NEHFRSKATLTIDKSSSTAYMQLSSITSEDSAVYYCARVYR---LGRY-FDYWGKGTMT 134  
 QY 121 VSS 123  
 DB 135 VSS 137

Search completed: September 9, 2004, 11:06:52  
 Job time : 9.9359 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 9, 2004, 11:01:20 ; Search time 37.8462 Seconds  
(without alignments)  
1025.434 Million cell updates/sec

Title: US-09-880-748-2\_COPY\_1\_123

Perfect score: 640  
Sequence: 1 QVQLQDSGAEVKKPKSSSVRV.....LFPHYGMDVWGRTWTVS 123

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

1 number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 70 summaries

Database :

1: SPREMBL.25.\*  
2: sp\_archaea.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp Vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvivirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	456.5	71.3	116	4 Q9UL89	Q9UL89 homo sapien
2	439.5	68.7	159	4 Q96GSO	Q96GSO homo sapien
3	403.5	63.0	124	4 Q9UL92	Q9UL92 homo sapien
4	391	-61.1	614	4 Q96GAS	Q96GAS homo sapien
5	390.5	61.0	496	4 Q96DKO	Q96DKO homo sapien
6	388	60.6	125	4 Q9UL95	Q9UL95 homo sapien
7	386	60.3	119	4 Q9UL94	Q9UL94 homo sapien
8	386	60.3	119	5 Q9GYZ2	Q9GYZ2 schistosoma
9	383.5	59.9	500	4 Q9BRV0	Q9BRV0 homo sapien
10	373.5	58.4	145	11 Q924O9	Q924O9 mus musculu
11	369.5	57.7	145	11 Q924O6	Q924O6 mus musculu
12	368.5	57.6	613	11 Q8YCX7	Q8YCX7 mus musculu
13	368	57.5	146	11 Q924Q3	Q924Q3 mus musculu
14	367	57.3	473	11 Q9D8L4	Q9D8L4 mus musculu
15	363	56.7	150	4 Q9Y298	Q9Y298 homo sapien
16	362.5	56.6	463	11 Q99LC4	Q99LC4 mus musculu

# ALIGNMENTS

17	361	56.4	497	4 Q8WY24	Q8WY24 homo sapien
18	360.5	56.3	145	11 Q924P7	Q924P7 mus musculu
19	360	56.2	117	11 Q9QX89	Q9QX89 mus musculu
20	359.5	56.2	143	11 Q924R0	Q924R0 mus musculu
21	359.5	56.2	145	11 Q924R4	Q924R4 mus musculu
22	357.5	55.9	143	11 Q924Q5	Q924Q5 mus musculu
23	357	55.8	168	11 Q8VDC9	Q8VDC9 mus musculu
24	356.5	55.7	145	11 Q924R1	Q924R1 mus musculu
25	355.5	55.5	482	11 Q8K172	Q8K172 mus musculu
26	354.5	55.4	473	11 Q99L25	Q99L25 mus musculu
27	354	55.3	146	11 Q924R8	Q924R8 mus musculu
28	353.5	55.2	143	11 Q924R0	Q924R0 mus musculu
29	353.5	55.2	145	11 Q924R3	Q924R3 mus musculu
30	353.5	55.2	145	11 Q924O7	Q924O7 mus musculu
31	352.5	55.1	118	11 Q921C4	Q921C4 mus musculu
32	352.5	55.1	143	11 Q924R7	Q924R7 mus musculu
33	352	55.0	140	11 Q924R2	Q924R2 mus musculu
34	352	55.0	614	11 Q7TMT6	Q7TMT6 mus musculu
35	351.5	54.9	141	11 Q924Q4	Q924Q4 mus musculu
36	351.5	54.9	143	11 Q91V67	Q91V67 mus musculu
37	351	54.8	142	11 Q924Q1	Q924Q1 mus musculu
38	350.5	54.8	469	4 Q7Z7P5	Q7Z7P5 homo sapien
39	350	54.7	117	11 Q9QXFO	Q9QXFO mus musculu
40	348	54.4	140	11 Q924P8	Q924P8 mus musculu
41	347.5	54.3	143	11 Q91VA2	Q91VA2 mus musculu
42	347	54.2	144	11 Q924P5	Q924P5 mus musculu
43	347	54.2	181	11 Q91WT1	Q91WT1 mus musculu
44	346.5	54.1	143	11 Q924P9	Q924P9 mus musculu
45	346.5	54.1	241	11 Q921A6	Q921A6 mus musculu
46	346	54.1	142	11 Q924Q2	Q924Q2 mus musculu
47	344.5	53.8	137	11 Q924R6	Q924R6 mus musculu
48	344	53.8	468	11 Q924R3	Q924R3 mus musculu
49	342.5	53.5	139	11 Q924R5	Q924R5 mus musculu
50	342.5	53.5	243	11 Q7TQM2	Q7TQM2 mus musculu
51	342	53.4	146	11 Q924Q8	Q924Q8 mus musculu
52	342	53.4	147	11 Q925S3	Q925S3 mus musculu
53	342	53.4	480	11 Q8K0Z4	Q8K0Z4 mus musculu
54	341	53.3	470	11 Q7TMM1	Q7TMM1 mus musculu
55	340	53.1	123	11 Q8V111	Q8V111 mus musculu
56	339	53.0	474	11 Q8R3H6	Q8R3H6 mus musculu
57	338	52.8	120	11 Q920E8	Q920E8 mus musculu
58	337.5	52.7	278	11 Q921K1	Q921K1 mus musculu
59	337.5	52.7	488	11 Q8K0P2	Q8K0P2 mus musculu
60	335	52.3	484	11 Q99LA6	Q99LA6 mus musculu
61	331	51.7	157	4 Q95978	Q95978 homo sapien
62	331	51.7	489	11 Q8VXC4	Q8VXC4 mus musculu
63	330.5	51.6	109	11 Q9JL75	Q9JL75 mus musculu
64	328.5	51.3	488	11 Q91WR1	Q91WR1 mus musculu
65	326.5	51.0	110	11 Q9JL77	Q9JL77 mus musculu
66	324.5	50.7	143	11 Q924R6	Q924R6 mus musculu
67	322.5	50.4	110	11 Q9UL83	Q9UL83 mus musculu
68	322.5	50.4	136	11 Q7TPE3	Q7TPE3 mus musculu
69	320	50.0	481	11 Q91WT3	Q91WT3 mus musculu
70	319	49.8	111	11 Q9D9B8	Q9D9B8 mus musculu

RESULT 1  
Q9UL89 PRELIMINARY; PRT; 116 AA.

AC Q9UL89; 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
(Fragment)  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_Taxid=9606;  
RN (1)

RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035025; AAD56261.1; -.  
DR HSSP; P01810; 2FB4.  
DR InterPro; IPR007110; Ig\_1like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1 16  
FT TER 116  
SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

Query Match 71.3%; Score 456.5; DB 4; Length 116;  
Best Local Similarity 76.3%; Pred. No. 1.1e-40; Mismatches 14; Indels 3; Gaps 1;  
Matches 90; Conservative 11; Mismatches 14; Indels 3; Gaps 1;  
QY 6 QSGAEVKKPGSSVRYSCKASGCTFNNNAIMVYQAPQGLEWMGGIIPMGSTAKYQNFQ 65  
DB 2 QSGAEVKKPGSSVRYSCKASGCTFNNNAIMVYQAPQGLEWMGGIIPMGSTAKYQNFQ 61  
QY 66 GCAVATADSTSTASMSLSLRSEDTAVYVCARSDLLLPHYGMDVWGRGTMVYSS 123  
DB 62 GCAVATADSTSTASMSLSLRSEDTAVYVCARSDLLLPHYGMDVWGRGTMVYSS 116

RESULT 2  
Q96GSO PRELIMINARY; PRT; 159 AA.  
ID Q96GSO  
AC Q96GSO;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Putative matrix cell adhesion molecule-3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCB1\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tilson M.D.;  
RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3  
RT mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3)."  
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY039025; AK82649.1; -.  
DR InterPro; IPR007110; Ig\_1like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 68.7%; Score 439.5; DB 4; Length 159;  
Best Local Similarity 66.9%; Pred. No. 1.1e-38; Mismatches 21; Indels 7; Gaps 1;  
Matches 87; Conservative 15; Mismatches 21; Indels 7; Gaps 1;  
QY 1 QVQLQSGAEVKKPGSSVRYSCKASGCTFNNNAIMVYQAPQGLEWMGGIIPMGSTAKY 60  
DB 20 QVQLVSGAEVKKPGSSVRYSCKASGCTFNNNAIMVYQAPQGLEWMGGIIPMGSTAKY 79  
QY 61 SQNFGRAVATADSTSTASMSLSLRSEDTAVYVCARSDLLLPHYGMDVW 113  
DB 80 SQNFGRAVATADSTSTASMSLSLRSEDTAVYVCARSDLLLPHYGMDVW 139  
QY 114 GRCITMTVSS 123  
DB 140 GCGITVTVSS 149

RESULT 3  
Q9UL92 PRELIMINARY; PRT; 124 AA.  
ID Q9UL92  
AC Q9UL92;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCB1\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035022; AAD56258.1; -.  
DR HSSP; P01772; 2FB4.  
DR InterPro; IPR007110; Ig\_1like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1 124  
FT TER 124  
SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 63.0%; Score 403.5; DB 4; Length 124;  
Best Local Similarity 65.3%; Pred. No. 5.2e-35; Mismatches 25; Indels 1; Gaps 1;  
Matches 81; Conservative 17; Mismatches 25; Indels 1; Gaps 1;  
QY 1 QVQLQSGAEVKKPGSSVRYSCKASGCTFNNNAIMVYQAPQGLEWMGGIIPMGSTAKY 60  
DB 1 EVQLVSGAEVKKPGSSVRYSCKASGCTFNNNAIMVYQAPQGLEWMGGIIPMGSTAKY 60  
QY 61 SQNFGRAVATADSTSTASMSLSLRSEDTAVYVCARSDLLLPHYGMDVWGRGTMV 119  
DB 61 AQKFGRAVATADSTSTASMSLSLRSEDTAVYVCARSDLLLPHYGMDVWGRGTMV 120  
QY 120 TVSS 123  
DB 121 TVSS 124

RESULT 4  
Q96GA6 PRELIMINARY; PRT; 614 AA.  
ID Q96GA6  
AC Q96GA6;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCB1\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tilson M.D.;  
RT "Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RT EMBL; BC009851; AA09851.1; -.  
DR PIR; S15590; S15590.  
DR GO; GO:0005622; C:intracellular; IEA.  
DR GO; GO:0003700; P:transcription factor activity; IEA.  
DR GO; GO:0003555; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR000005; HTHATAC.



DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_5.  
 DR SMART: SM00406; IGV\_1.  
 DR PROSITE: PS00041; HTH\_ARAC\_FAMILY\_1; 1.  
 DR PROSITE: PS50835; Ig\_LIKE; 5.  
 DR PROSITE: PS00290; IG\_MHC; 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 614 AA; 67921 MW; 55EFS36E77A9BBB CRC64;

Query Match 61.1%; Score 391; DB 4; Length 614;  
 Best Local Similarity 62.8%; Pred. No. 8e-33;  
 Matches 81; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

QY 1 QVLOOQSGAEVKKPGSSVYVSCASGCTFNNAIINWVROAPGQGLEMGIIIPMGSTAKY 60  
 DB 20 QVLOVSGAEVKKPGSSVYVSCASGCTFTYRYLIHWVROAPGQGLEMGIIIPFNQNTY 79  
 61 SQNFGQVAVITADESTSTASMEISLRSEDTAVYVCARSDLLPFHY-----GMDVWG 114  
 80 AQCFQDRTVITTRDRSMNTAYMELSLRSEDTAVYTCARG-----YSSWDPAFDIWG 131

QY 115 RGTMTVSS 123  
 DB 132 QGTMTVSS 140

RESULT 5  
 Q96DKO PRELIMINARY; PRT; 496 AA.

AC Q96DKO; PRELIMINARY; PRT; 496 AA.  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein FLJ25298.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.  
 RC TISSUE=caecic mucosa;  
 RA Ishihashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,  
 RA Hottu T., Hirooka S., Murakawa K., Takiguchi S., Kusano J., Chita Y.,  
 RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamaehita H., Chita Y.,  
 RA Sugiyama T., Irie R., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,  
 RA Kawakami B., Nagai K., Isegai T., Sugano S.,  
 "NEO human cDNA sequencing project."  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AK058027; BAB71633.1; -.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_4.  
 DR SMART: SM00406; IGV\_1.  
 DR PROSITE: PS50835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 496 AA; 53532 MW; C72E1E247C86FDC CRC64;

Query Match 61.0%; Score 390.5; DB 4; Length 496;  
 Best Local Similarity 60.5%; Pred. No. 6.9e-33;  
 Matches 78; Conservative 13; Mismatches 27; Indels 11; Gaps 2;

QY 1 QVLOOQSGAEVKKPGSSVYVSCASGCTFNNAIINWVROAPGQGLEMGIIIPMGSTAKY 60  
 DB 20 QVHLVSGAEVKKPGSSVYVSCASANMFRSYAFTVVRQAPGQGLEMGIIIPNFGAPY 79  
 QY 61 SQNFGQVAVITADESTSTASMEISLRSEDTAVYVCARSDLLPFHYG-----MDVWG 114  
 DB 80 AQNFDRTVITADSDTTTVMELSLRSEDTAVYTCARG-----LTVYSGSGSYVYLQHWG 134

QY 115 RGTMTVSS 123  
 DB 135 QGTMTVSS 143

RESULT 6  
 Q9UL95 PRELIMINARY; PRT; 125 AA.

AC Q9UL95; PRELIMINARY; PRT; 125 AA.  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus."  
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
 DR EMBL: AF035019; AAD56255.1; -.  
 DR HSSP: P01810; 2FBU.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV\_1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 125  
 SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 60.6%; Score 388; DB 4; Length 125;  
 Best Local Similarity 63.2%; Pred. No. 2.3e-33;  
 Matches 79; Conservative 14; Mismatches 30; Indels 2; Gaps 1;

QY 1 QVLOOQSGAEVKKPGSSVYVSCASGCTFNNAIINWVROAPGQGLEMGIIIPMGSTAKY 60  
 DB 1 EVQLVSGAEVKKPGASVYVSCASGYTFTYRYLIHWVROAPGQGLEMGIIIPNCGTNY 60  
 QY 61 SQNFGQVAVITADESTSTASMEISLRSEDTAVYVCARSR--DLLLPHYGMDVWGRGTM 118  
 DB 61 AQVQGRVAVITADTTISTAYMELSLRSDPTAVYVCARSGGGRIAAAGDAFDIWGQGTM 120

QY 119 VTVSS 123  
 DB 121 VTVSS 125

RESULT 7

Q9UL94 PRELIMINARY; PRT; 119 AA.

AC Q9UL94; PRELIMINARY; PRT; 119 AA.  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,  
 RA Young D.C.;

```

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035020; AAD56256.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16 CRC64;

Query Match 60.3%; Score 386; DB 4; Length 119;
Best Local Similarity 64.2%; Pred. No. 3.6e-33;
Matches 79; Conservative 13; Mismatches 27; Indels 4; Gaps 1;

1 QVQLQSGAEVKKPGSSVSVCKASGTFNNNAIMVVRQAPQGLEWMGIIIMFGTAKY 60
1 EVQLVESGAEVKKPGASVSVCKASGYTFTGYMMWRQAPQGLEWMGIMPNSTVINY 60
QY 61 SONFGRAVIAIDESTIASMELSLRSEDIAVYYCARSDLLFPHYGMDVWGRTVMT 120
Db 61 AKFGQKVTMTKDTSTIAYMELSRSDIAVYYCARSGRGLW----FDPWGQGLTIVT 116
QY 121 VSS 123
Db 117 VSS 119

RESULT 8
Q9GYZ2 PRELIMINARY; PRT; 119 AA.
ID Q9GYZ2;
AC Q9GYZ2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
DE (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidae;
OC Schistosomatidae; Schistosomidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum."
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF282622; AAG01452.1; -.
DR HSSP; P01772; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FDF5FA6AB CRC64;

Query Match 60.3%; Score 386; DB 5; Length 119;
Best Local Similarity 63.4%; Pred. No. 3.6e-33;
Matches 78; Conservative 13; Mismatches 28; Indels 4; Gaps 1;

1 QVQLQSGAEVKKPGSSVSVCKASGTFNNNAIMVVRQAPQGLEWMGIIIMFGTAKY 60
1 QVQLVESGAEVKKPGASVSVCKASGYTFTGYMMWRQAPQGLEWMGIMPNSTVINY 60
QY 61 SONFGRAVIAIDESTIASMELSLRSEDIAVYYCARSDLLFPHYGMDVWGRTVMT 120
Db 61 NQFDFRVTMTYDKSFSFYMDLSIRSDASAVYCARYYD----DHYCLDYWGQGLTIVT 116

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QY 121 VSS 123
Db 117 VSS 119

RESULT 9
Q9BRV0 PRELIMINARY; PRT; 500 AA.
ID Q9BRV0;
AC Q9BRV0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RT TISSUE=prostate;
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC005951; AAH05951.1; -.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 59.9%; Score 383.5; DB 4; Length 500;
Best Local Similarity 60.3%; Pred. No. 3.9e-32;
Matches 79; Conservative 12; Mismatches 29; Indels 11; Gaps 2;

1 QVQLQSGAEVKKPGSSVSVCKASGTFNNNAIMVVRQAPQGLEWMGIIIMFGTAKY 60
20 QVHLVQSGAEVSPASVSVCKTSGYAFHYTSITVWQAPQGLEWMGIMWSPSSDNTRF 79
QY 61 SONFGRAVIAIDESTIASMELSLRSEDIAVYYCAR-----SRDLLFPHYGMDV 112
Db 80 AKFGQKVTMTKDTSTIAYMELSRSDIAVYYCARCYSCSQND---YTYTMDV 136
QY 113 WGRGTVTVSS 123
Db 137 WKGKTVTVSS 147

RESULT 10
Q924Q9 PRELIMINARY; PRT; 145 AA.
ID Q924Q9;
AC Q924Q9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kozono Y., Kozono H., Azuma T.;
RC STRAIN=C57BL/6;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP)."
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
EMBL; AB067791; BAB63276.1; -.

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DR PIR: F28833; F28833.  
DR PIR: F33932; F33932.  
DR PIR: PH1105; PH1105.  
DR PIR: PH1108; PH1108.  
DR PIR: PH1114; PH1114.  
DR PIR: PH1118; PH1118.  
DR PIR: PH1119; PH1119.  
DR PIR: PH1125; PH1125.  
DR PIR: PH1126; PH1126.  
DR PIR: PH1128; PH1128.  
DR PIR: PH1129; PH1129.  
DR PIR: PH1131; PH1131.  
DR PIR: PH1133; PH1133.  
DR PIR: PH1137; PH1137.  
DR PIR: PH1139; PH1139.  
DR PIR: PH1142; PH1142.  
DR PIR: PH1144; PH1144.  
DR PIR: PH1147; PH1147.  
DR PIR: PH1149; PH1149.  
DR PIR: PH1150; PH1150.  
DR PIR: PH1151; PH1151.  
DR PIR: PH1152; PH1152.  
DR PIR: PH1153; PH1153.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003596; IG\_v.  
DR Pfam: PF00047; IG\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1 145 145  
SQ SEQUENCE 145 AA; 16001 MW; 0F409EB09FA33D2 CRC64;

Query Match 58.4%; Score 373.5; DB 11; Length 145;  
Best Local Similarity 58.5%; Pred. No. 9.8e-32;  
Matches 72; Conservative 22; Mismatches 26; Indels 3; Gaps 1;

QY 1 QVQLQSGAEVKKPGSSVRVSCKASGCTFNNNAINWVROAPQGGLFMWGIIIPMGATAY 60  
DB 1 QVQLQPGAEIVKPGASVSLSCASGYTFTSYMMHWKQRPGRGLEWIGRIDPNSGCTY 60  
QY 61 SONFGQVAITADESTSTSMELSLRSEDTAVYYCARSRDLLLPHYGMDVWGRTWY 120  
DB 61 NEKFSKATLTVDKPESTAVYQWLSLTSEDSAVYYCARSL--LTITYAMDYWGQTSVT 117

QY 121 VSS 123  
DB 118 VSS 120

AC 092406 PRELIMINARY; PRT; 145 AA.  
AC 092406; 01-DEC-2001 (T-EMBLrel. 19, Created)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
DE 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
DE VHL86.2-D-U-C mu protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RA Kozono Y., Kozono H., Azuma T.;  
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
RT Affinity Maturation of B Cell Antigen Receptors in Response to (-  
RT Hydroxy-3-Nitrophenyl)Acetyl (NP)";  
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB067794; BAB63279.1; -;  
DR PIR; F28833; F28833.  
DR PIR; F33932; F33932.  
DR PIR; PH1105; PH1105.

DR PIR: PH1108; PH1108.  
DR PIR: PH1114; PH1114.  
DR PIR: PH1118; PH1118.  
DR PIR: PH1119; PH1119.  
DR PIR: PH1125; PH1125.  
DR PIR: PH1126; PH1126.  
DR PIR: PH1128; PH1128.  
DR PIR: PH1129; PH1129.  
DR PIR: PH1131; PH1131.  
DR PIR: PH1133; PH1133.  
DR PIR: PH1137; PH1137.  
DR PIR: PH1139; PH1139.  
DR PIR: PH1142; PH1142.  
DR PIR: PH1144; PH1144.  
DR PIR: PH1147; PH1147.  
DR PIR: PH1149; PH1149.  
DR PIR: PH1150; PH1150.  
DR PIR: PH1151; PH1151.  
DR PIR: PH1152; PH1152.  
DR PIR: PH1153; PH1153.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003596; IG\_v.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1 145 145  
SQ SEQUENCE 145 AA; 16011 MW; 9BC0846D40DF97EA CRC64;

Query Match 57.7%; Score 369.5; DB 11; Length 145;  
Best Local Similarity 58.5%; Pred. No. 2.6e-31;  
Matches 72; Conservative 21; Mismatches 27; Indels 3; Gaps 1;

QY 1 QVQLQSGAEVKKPGSSVRVSCKASGCTFNNNAINWVROAPQGGLFMWGIIIPMGATAY 60  
DB 1 QVQLQPGAEIVKPGASVSLSCASGYTFTSYMMHWKQRPGRGLEWIGRIDPNSGCTY 60  
QY 61 SONFGQVAITADESTSTSMELSLRSEDTAVYYCARSRDLLLPHYGMDVWGRTWY 120  
DB 61 NEKFSKATLTVDKPESTAVYQWLSLTSEDSAVYYCARSL--LTITYAMDYWGQTSVT 117

QY 121 VSS 123  
DB 118 VSS 120

AC 08VCX7 PRELIMINARY; PRT; 613 AA.  
AC 08VCX7; 01-MAR-2002 (T-EMBLrel. 20, Created)  
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)  
DE 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN IGH-6.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Salivary gland;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC018315; AAH18315.1; -;  
DR MGD; MGJ:96448; Igh-6.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_v.  
DR Pfam; PF00047; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.

KW Hypothetical protein.  
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;  
Query Match 57.6%; Score 368.5; DB 11; Length 613;  
Best Local Similarity 58.5%; Pred. No. 2e-30;  
Matches 72; Conservative 19; Mismatches 27; Indels 5; Gaps 1;  
QY 1 QVQLQSGAEVKKPKSSVAVSCASGCTFNNNAIMVVRQAPQGLEWMGCIIPMEGTAKY 60  
DB 20 QVQLQSGAEVKKPKSSVAVSCASGCTFNNNAIMVVRQAPQGLEWMGCIIPMEGTAKY 79  
QY 61 SONFGKVAITADESTTASMEISLRSEDPTAVYICARSRLDLPFHGMVWGRTWYT 120  
DB 80 NEKFKGKATFTADTSNTAYMQLSLTSEDSAVYICARLGRWYF-----DVMGAGTIVT 134  
QY 121 VSS 123  
DB 135 VSS 137  
RESULT 13  
ID Q924Q3 PRELIMINARY; PRT; 146 AA.  
AC Q924Q3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE VHL6.2-D-C-mu protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RA Kozono Y., Kozono H., Azuma T.;  
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
RT Hydroxy-3-nitrophenyl)Acetyl (NP) ".  
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB067797; BAB63282.1; -  
DR PIR; F28833; F28833.  
DR PIR; F33932; F33932.  
DR PIR; PH1105; PH1105.  
DR PIR; PH1108; PH1108.  
DR PIR; PH1114; PH1114.  
DR PIR; PH1118; PH1118.  
DR PIR; PH1119; PH1119.  
DR PIR; PH1125; PH1125.  
DR PIR; PH1126; PH1126.  
DR PIR; PH1128; PH1128.  
DR PIR; PH1129; PH1129.  
DR PIR; PH1131; PH1131.  
DR PIR; PH1134; PH1134.  
DR PIR; PH1137; PH1137.  
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DR PIR; PH1142; PH1142.  
DR PIR; PH1144; PH1144.  
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DR PIR; PH1149; PH1149.  
DR PIR; PH1150; PH1150.  
DR PIR; PH1151; PH1151.  
DR PIR; PH1152; PH1152.  
DR PIR; PH1153; PH1153.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
FT PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 146 146  
SQ SEQUENCE 146 AA; 16136 MW; CEA8DD6E1955807F CRC64;

Query Match 57.5%; Score 368; DB 11; Length 146;  
Best Local Similarity 58.5%; Pred. No. 3.8e-31;  
Matches 72; Conservative 21; Mismatches 28; Indels 2; Gaps 1;  
QY 1 QVQLQSGAEVKKPKSSVAVSCASGCTFNNNAIMVVRQAPQGLEWMGCIIPMEGTAKY 60  
DB 1 QVQLQSGAEVKKPKSSVAVSCASGCTFNNNAIMVVRQAPQGLEWMGCIIPMEGTAKY 60  
QY 61 SONFGKVAITADESTTASMEISLRSEDPTAVYICARSRLDLPFHGMVWGRTWYT 120  
DB 61 NEKFKGKATFTADTSNTAYMQLSLTSEDSAVYICARS--LYDGDYAMDYWGQTSVT 118  
QY 121 VSS 123  
DB 119 VSS 121  
RESULT 14  
ID Q9DBL4 PRELIMINARY; PRT; 473 AA.  
AC Q9DBL4;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE 181060009R1K protein.  
CN IGH-1 OR 181060009R1K.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Glass C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsumoto Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bul C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RT Nature 409:685-690(2001).  
DR EMBL; AK007918; BAB25349.1; -  
DR PIR; S26746; S26746.  
DR HSSP; P01842; 7PAB.  
DR MGD; MGI:96443; Igh-1.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;  
Query Match 57.3%; Score 367; DB 11; Length 473;  
Best Local Similarity 57.9%; Pred. No. 2.1e-30;  
Matches 73; Conservative 22; Mismatches 21; Indels 10; Gaps 2;  
QY 1 QVQLQSGAEVKKPKSSVAVSCASGCTFNNNAIMVVRQAPQGLEWMGCIIPMEGTAKY 60  
DB 1 QVQLQSGAEVKKPKSSVAVSCASGCTFNNNAIMVVRQAPQGLEWMGCIIPMEGTAKY 60

Db 20 QVQLKQSGAEIVKPGASVKISCKASGYTFDYIYNMKQRPQGQLEWIGKIGPGSGSTYY 79  
QY 61 SQNFOGRVATITAPDSTSTASMEISLSRSEPTAVYYCARSDLLFPHYGMD---VWGSGT 117  
Db 80 NEKFKGATITFADKSSSTAYTQLSLSLSEDAVYPCARS-----GYDWMFAYWGQGT 132  
QY 118 MVTVSS 123  
Db 133 LVTVSA 138

## RESULT 15

Q9Y298

ID Q9Y298 PRELIMINARY; PRT; 150 AA.

AC Q9Y298;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE IGG VH protein precursor (Fragment).

IGG VH.

Homo sapiens (human);

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI TaxID=9606;

[1]

SEQUENCE FROM N.A.

MEDLINE=98322155; Pubmed=9657749;

Jaquemin M.G., Vander Elst L.P.L.;

"Mechanism and kinetics of factor VIII inactivation: study with an

RT IGG4 monoclonal antibody derived from a hemophilia A patient with

inhibitor."

Blood 92:496-506 (1998).

EMBL: AJ224083; CAA11829.1; -.

HSP; P01772; 2PB4.

GO: GO:0005887; C: integral to plasma membrane; NAS.

GO: GO:0016489; F: immunoglobulin receptor activity; NAS.

GO: GO:0016066; P: cellular defense response (sensu Vertebrata); NAS.

InterPro: IPR007110; IG-like.

InterPro: IPR003596; IG\_v.

Pfam: PF00047; Ig; 1.

SMART; SM00406; IgV; 1.

PROSITE; PS50835; IG\_LIKE; 1.

Signal.

FT SIGNAL. 1 19 POTENTIAL.

FT NON\_TER 150 150

SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

## Query Match

Best Local Similarity 56.7%; Score 363; DB 4; Length 150;

Matches 74; Conservative 14; Mismatches 29; Indels 6; Gaps 1;

QY 1 QVQLKQSGAEIVKPGASVKISCKASGYTFDYIYNMKQRPQGQLEWIGKIGPGSGSTYY 60  
Db 20 QVQLKQSGAEIVKPGASVKISCKASGYTFDYIYNMKQRPQGQLEWIGKIGPGSGSTYY 79  
QY 61 SQNFOGRVATITAPDSTSTASMEISLSRSEPTAVYYCARSDLLFPHYGMD---VWGSGT 120  
Db 80 NEKFKGATITFADKSSSTAYTQLSLSLSEDAVYPCARS-----GYDWMFAYWGQGT 133  
QY 121 VSS 123  
Db 134 VSS 136

Search completed: September 9, 2004, 11:08:43  
Job time : 39.8462 secs

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## OM protein - protein search, using sw model

Run on: September 9, 2004, 10:53:58 ; Search time 47.9103 Seconds

(without alignments)  
654.615 Million cell updates/sec

Title: US-09-880-748-2\_COPY\_139\_249

Perfect score: 585  
Sequence: 1 AFSSSELTQDPAAVSAVALGQTV.....RDSGNHWVFGGTELTIVG 111Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

1 number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 70 summaries

## Database :

A\_Geneseq\_29u04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	585	100.0	248	5	ABP44336 Human Bly
2	585	100.0	248	5	ABP44586 Human Bly
3	585	100.0	248	5	ABP44343 Human Bly
4	585	100.0	248	5	ABP44328 Human Bly
5	585	100.0	248	5	ABP44612 Human Bly
6	585	100.0	249	5	ABP44344 Human Bly
7	585	100.0	249	5	ABP44348 Human Bly
8	585	100.0	249	5	ABP44350 Human Bly
9	585	100.0	249	5	ABP44432 Human Bly
10	585	100.0	249	5	ABP44451 Human Bly
11	585	100.0	249	5	ABP44477 Human Bly
12	585	100.0	249	5	ABP44497 Human Bly
13	585	100.0	249	5	ABP44548 Human Bly
14	585	100.0	249	5	ABP44613 Human Bly
15	585	100.0	249	5	ABP44621 Human Bly
16	585	100.0	249	5	ABP44644 Human Bly
17	585	100.0	249	5	ABP44660 Human Bly
18	585	100.0	249	5	ABP44664 Human Bly
19	585	100.0	249	5	ABP44701 Human Bly
20	585	100.0	249	5	ABP44710 Human Bly
21	585	100.0	249	5	ABP44732 Human Bly
22	585	100.0	249	5	ABP44747 Human Bly
23	585	100.0	249	5	ABP44756 Human Bly
24	585	100.0	249	5	ABP44760 Human Bly
25	585	100.0	249	5	ABP43991 Human Bly

26	585	100.0	249	5	ABP44321 Human Bly
27	585	100.0	249	5	ABP44327 Human Bly
28	585	100.0	249	5	ABP44333 Human Bly
29	585	100.0	249	5	ABP44374 Human Bly
30	585	100.0	249	5	ABP44387 Human Bly
31	585	100.0	249	5	ABP44401 Human Bly
32	585	100.0	249	5	ABP44452 Human Bly
33	585	100.0	249	5	ABP44487 Human Bly
34	585	100.0	249	5	ABP44493 Human Bly
35	585	100.0	249	5	ABP44506 Human Bly
36	585	100.0	249	5	ABP44509 Human Bly
37	585	100.0	249	5	ABP44526 Human Bly
38	585	100.0	249	5	ABP44553 Human Bly
39	585	100.0	249	5	ABP44652 Human Bly
40	585	100.0	249	5	ABP44662 Human Bly
41	585	100.0	249	5	ABP44685 Human Bly
42	585	100.0	249	5	ABP44722 Human Bly
43	585	100.0	249	5	ABP44770 Human Bly
44	585	100.0	249	5	ABP44794 Human Bly
45	585	100.0	249	5	ABP44810 Human Bly
46	585	100.0	249	5	ABP44376 Human Bly
47	585	100.0	249	5	ABP44389 Human Bly
48	585	100.0	249	5	ABP44393 Human Bly
49	585	100.0	249	5	ABP44397 Human Bly
50	585	100.0	249	5	ABP44411 Human Bly
51	585	100.0	249	5	ABP44448 Human Bly
52	585	100.0	249	5	ABP44457 Human Bly
53	585	100.0	249	5	ABP44463 Human Bly
54	585	100.0	249	5	ABP44488 Human Bly
55	585	100.0	249	5	ABP44505 Human Bly
56	585	100.0	249	5	ABP44561 Human Bly
57	585	100.0	249	5	ABP44596 Human Bly
58	585	100.0	249	5	ABP44603 Human Bly
59	585	100.0	249	5	ABP44636 Human Bly
60	585	100.0	249	5	ABP44647 Human Bly
61	585	100.0	249	5	ABP44705 Human Bly
62	585	100.0	249	5	ABP44724 Human Bly
63	585	100.0	249	5	ABP44740 Human Bly
64	585	100.0	249	5	ABP44743 Human Bly
65	585	100.0	249	5	ABP44753 Human Bly
66	585	100.0	249	5	ABP44765 Human Bly
67	585	100.0	249	5	ABP44346 Human Bly
68	585	100.0	249	5	ABP44388 Human Bly
69	585	100.0	249	5	ABP44398 Human Bly
70	585	100.0	249	5	ABP44422 Human Bly

## ALIGNMENTS

RESULT 1  
ABP44336  
ID ABP44336 standard; protein; 248 AA.  
XX  
AC ABP44336;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scFv SEQ ID 347.  
XX  
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX

PF 15-JUN-2001; 2001WO-US019110.  
XX  
XX 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
PI WPI; 2002-114799/15.  
XX  
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.  
XX  
XX Claim 1; Page 818-819; 3148pp; English.  
PS  
XX This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
XX Sequence 248 AA;  
SQ  
XX  
XX Query Match 100.0%; Score 585; DB 5; Length 248;  
Best Local Similarity 100.0%; Pred. No. 1e-36;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AFSSSELTDPDAVSVALGQTVRVTCQGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIP 60  
DB 138 AFSSSELTDPDAVSVALGQTVRVTCQGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIP 197  
61 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWFVGGTETLVLG 111  
198 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWFVGGTETLVLG 248  
DB  
XX  
XX RESULT 2  
XX ABP44586 standard; protein; 248 AA.  
XX ID ABP44586;  
XX AC ABP44586;  
XX XX  
XX DT 19-AUG-2002 (first entry)  
XX XX  
XX DE Human Blys binding scFv SEQ ID 597.  
XX XX  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX Homo sapiens.  
XX OS  
XX PN WO200202641-A1.

XX  
XX 10-JAN-2002.  
PD  
XX  
XX 15-JUN-2001; 2001WO-US019110.  
PF  
XX  
XX 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
PI WPI; 2002-114799/15.  
XX  
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.  
XX  
XX Claim 1; Page 1114-1115; 3148pp; English.  
PS  
XX This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
XX Sequence 248 AA;  
SQ  
XX  
XX Query Match 100.0%; Score 585; DB 5; Length 248;  
Best Local Similarity 100.0%; Pred. No. 1e-36;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AFSSSELTDPDAVSVALGQTVRVTCQGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIP 60  
DB 138 AFSSSELTDPDAVSVALGQTVRVTCQGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIP 197  
61 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWFVGGTETLVLG 111  
198 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWFVGGTETLVLG 248  
DB  
XX  
XX RESULT 3  
XX ABP44343 standard; protein; 248 AA.  
XX ID ABP44343;  
XX AC ABP44343;  
XX XX  
XX DT 19-AUG-2002 (first entry)  
XX XX  
XX DE Human Blys binding scFv SEQ ID 354.  
XX XX  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX



OS Homo sapiens.  
 XX PN WO200202641-A1.  
 XX PD 10-JAN-2002.  
 XX PF 15-JUN-2001; 2001WO-US019110.  
 XX PR 16-JUN-2000; 2000US-0212210P.  
 PR 17-OCT-2000; 2000US-0240816P.  
 PR 16-MAR-2001; 2001US-0276248P.  
 PR 21-MAR-2001; 2001US-027379P.  
 PR 25-MAY-2001; 2001US-0293499P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX WPI; 2002-114799/15.  
 PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
 PT diagnosis and treatment of cancers and immune disorders.  
 XX  
 PS Claim 1; Page 826-827; 3148pp; English.  
 XX  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumor necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent  
 CC the antibodies and fragments of the antibodies described in the method of  
 CC the invention  
 CC  
 XX SQ Sequence 248 AA;  
 Query Match 100.0%; Score 585; DB 5; Length 248;  
 Best Local Similarity 100.0%; Pred. No. 1e-36;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AFSSSELTDPNAVVALGQTVRTTCGDSLSRYSYASWYQOKPGQAPLVLYGKNNRPSGIP 60  
 DB 138 AFSSSELTDPNAVVALGQTVRTTCGDSLSRYSYASWYQOKPGQAPLVLYGKNNRPSGIP 197  
 QY 61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRSDSGNHVFGGTELTVLG 111  
 DB 198 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRSDSGNHVFGGTELTVLG 248  
 RESULT 4  
 ID ABP44328  
 ID ABP44328 standard; protein; 248 AA.  
 AC ABP44328;  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human Blys binding scFv SEQ ID 339.  
 XX  
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumor necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX  
 OS Homo sapiens.  
 XX PN WO200202641-A1.  
 XX PD 10-JAN-2002.  
 XX PF 15-JUN-2001; 2001WO-US019110.  
 XX PR 16-JUN-2000; 2000US-0212210P.  
 PR 17-OCT-2000; 2000US-0240816P.  
 PR 16-MAR-2001; 2001US-0276248P.  
 PR 21-MAR-2001; 2001US-027379P.  
 PR 25-MAY-2001; 2001US-0293499P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX WPI; 2002-114799/15.  
 PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
 PT diagnosis and treatment of cancers and immune disorders.  
 XX  
 PS Claim 1; Page 808-809; 3148pp; English.  
 XX  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumor necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent  
 CC the antibodies and fragments of the antibodies described in the method of  
 CC the invention  
 CC  
 XX SQ Sequence 248 AA;  
 Query Match 100.0%; Score 585; DB 5; Length 248;  
 Best Local Similarity 100.0%; Pred. No. 1e-36;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AFSSSELTDPNAVVALGQTVRTTCGDSLSRYSYASWYQOKPGQAPLVLYGKNNRPSGIP 60  
 DB 138 AFSSSELTDPNAVVALGQTVRTTCGDSLSRYSYASWYQOKPGQAPLVLYGKNNRPSGIP 197  
 QY 61 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRSDSGNHVFGGTELTVLG 111  
 DB 198 DRFSGSSSGNTASLTITGAQAEDEADYYCNSRSDSGNHVFGGTELTVLG 248  
 RESULT 5  
 ID ABP44612  
 ID ABP44612 standard; protein; 248 AA.  
 AC ABP44612;  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human Blys binding scFv SEQ ID 623.  
 XX  
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KM common variable immunodeficiency; acquired immunodeficiency syndrome.  
OS Homo sapiens.  
XX  
XX MO200202641-A1.  
XX  
XX 10-JAN-2002.  
XX  
XX 15-JUN-2001; 2001WO-US019110.  
XX  
XX 16-JUN-2000; 2000US-0212210P.  
XX 17-OCT-2000; 2000US-0240816P.  
XX 16-MAR-2001; 2001US-0276248P.  
XX 21-MAR-2001; 2001US-0277379P.  
XX 25-MAY-2001; 2001US-0293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
XX diagnosis and treatment of cancers and immune disorders.  
XX  
XX Claim 1; Page 1145-1146; 3148pp; English.  
XX  
XX This invention describes novel antibodies that immunospecifically bind to  
XX B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the  
XX tumour necrosis factor (TNF) super family and induces B cell  
XX proliferation and differentiation. The antibodies of the invention have  
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
XX antirheumatic and antiAIDS activity and can be used in vaccines to  
XX inhibit the expression and activity of BLyS. The antibodies bind to BLyS  
XX and so may be used to detect and quantitate the presence of BLyS in  
XX biological samples and may be used in this way to diagnose disease  
XX associated with aberrant expression of BLyS. They may also be  
XX administered to treat diseases associated with aberrant BLyS expression  
XX and activity such as cancer, immune, and autoimmune disorders and  
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
XX the antibodies and fragments of the antibodies described in the method of  
XX the invention  
SQ Sequence 248 AA;  
Query Match 100.0%; Score 585; DB 5; Length 248;  
Best Local Similarity 100.0%; Pred. NO. 1e-36;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AFSSSETDPAVVALGQTVAVTCQGSLSRYASVWYQOKRQAPVLYTYGKNNRPSGIP 60  
DB 139 AFSSSETDPAVVALGQTVAVTCQGSLSRYASVWYQOKRQAPVLYTYGKNNRPSGIP 197  
QY 61 DRFGSSSGNTASLTITGAQAEADADYCNRSRDSGNHNVFGGTELTVLG 111  
DB 198 DRFGSSSGNTASLTITGAQAEADADYCNRSRDSGNHNVFGGTELTVLG 248  
RESULT 6  
ID ABP44344 standard; protein; 249 AA.  
XX  
XX ABP44344;  
AC  
XX  
XX 19-AUG-2002 (first entry)  
XX

DE Human BLyS binding scFv SEQ ID 355.  
XX  
XX BLyS; B lymphocyte stimulator; TNF superfamily; human; cyostatic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
OS Homo sapiens.  
XX  
XX MO200202641-A1.  
XX  
XX 10-JAN-2002.  
XX  
XX 15-JUN-2001; 2001WO-US019110.  
XX  
XX 16-JUN-2000; 2000US-0212210P.  
XX 17-OCT-2000; 2000US-0240816P.  
XX 16-MAR-2001; 2001US-0276248P.  
XX 21-MAR-2001; 2001US-0277379P.  
XX 25-MAY-2001; 2001US-0293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
XX diagnosis and treatment of cancers and immune disorders.  
XX  
XX Claim 1; Page 827-828; 3148pp; English.  
XX  
XX This invention describes novel antibodies that immunospecifically bind to  
XX B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the  
XX tumour necrosis factor (TNF) super family and induces B cell  
XX proliferation and differentiation. The antibodies of the invention have  
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
XX antirheumatic and antiAIDS activity and can be used in vaccines to  
XX inhibit the expression and activity of BLyS. The antibodies bind to BLyS  
XX and so may be used to detect and quantitate the presence of BLyS in  
XX biological samples and may be used in this way to diagnose disease  
XX associated with aberrant expression of BLyS. They may also be  
XX administered to treat diseases associated with aberrant BLyS expression  
XX and activity such as cancer, immune, and autoimmune disorders and  
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
XX the antibodies and fragments of the antibodies described in the method of  
XX the invention  
SQ Sequence 249 AA;  
Query Match 100.0%; Score 585; DB 5; Length 249;  
Best Local Similarity 100.0%; Pred. NO. 1e-36;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AFSSSETDPAVVALGQTVAVTCQGSLSRYASVWYQOKRQAPVLYTYGKNNRPSGIP 60  
DB 139 AFSSSETDPAVVALGQTVAVTCQGSLSRYASVWYQOKRQAPVLYTYGKNNRPSGIP 198  
QY 61 DRFGSSSGNTASLTITGAQAEADADYCNRSRDSGNHNVFGGTELTVLG 111  
DB 199 DRFGSSSGNTASLTITGAQAEADADYCNRSRDSGNHNVFGGTELTVLG 249  
RESULT 7  
ID ABP44348 standard; protein; 249 AA.  
XX  
XX ABP44348;  
AC

XX 19-AUG-2002 (first entry)  
DT Human Blys binding scFv SEQ ID 359.  
XX  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
DE immunosuppressive; immunostimulant; immunomodulatory; antithumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
OS Homo sapiens.  
XX  
XX WO200202641-A1.  
PN  
XX 10-JAN-2002.  
PD  
XX 15-JUN-2001; 2001WO-US019110.  
PF  
XX 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX  
XX WPI; 2002-114799/15.  
XX  
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.  
XX  
XX Claim 1; Page 832-833; 3148pp; English.  
XX  
XX This invention describes novel antibodies that immunospecifically bind to  
XX B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
XX tumour necrosis factor (TNF) super family and induces B cell  
XX proliferation and differentiation. The antibodies of the invention have  
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
XX antithumatic and antiAIDS activity and can be used in vaccines to  
XX inhibit the expression and activity of Blys. The antibodies bind to Blys  
XX and so may be used to detect and quantitate the presence of Blys in  
XX biological samples and may be used in this way to diagnose disease  
XX associated with aberrant expression of Blys. They may also be  
XX administered to treat diseases associated with aberrant Blys expression  
XX and activity such as cancer, immune, and autoimmune disorders and  
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
XX the antibodies and fragments of the antibodies described in the method of  
XX the invention  
XX  
XX Sequence 249 AA;  
SQ  
Query Match 100.0%; Score 585; DB 5; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1e-36;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AFSSSETLDPANVVALGQTVRVTCQDLSRSYASWYQKPGQAPLVLYGKNNRSGIP 60  
DB 139 AFSSSETLDPANVVALGQTVRVTCQDLSRSYASWYQKPGQAPLVLYGKNNRSGIP 198  
QY 61 DRFGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFGGTETLVLG 111  
DB 199 DRFGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFGGTETLVLG 249  
RESULT 8  
ABP44350

ID ABP44350 standard; protein; 249 AA.  
XX  
XX AC ABP44350;  
XX  
XX 19-AUG-2002 (first entry)  
DT Human Blys binding scFv SEQ ID 361.  
XX  
XX DE Human Blys binding scFv SEQ ID 361.  
XX  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antithumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
OS Homo sapiens.  
XX  
XX WO200202641-A1.  
PN  
XX 10-JAN-2002.  
PD  
XX 15-JUN-2001; 2001WO-US019110.  
PF  
XX 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX  
XX WPI; 2002-114799/15.  
XX  
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.  
XX  
XX Claim 1; Page 834-835; 3148pp; English.  
XX  
XX This invention describes novel antibodies that immunospecifically bind to  
XX B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
XX tumour necrosis factor (TNF) super family and induces B cell  
XX proliferation and differentiation. The antibodies of the invention have  
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
XX antithumatic and antiAIDS activity and can be used in vaccines to  
XX inhibit the expression and activity of Blys. The antibodies bind to Blys  
XX and so may be used to detect and quantitate the presence of Blys in  
XX biological samples and may be used in this way to diagnose disease  
XX associated with aberrant expression of Blys. They may also be  
XX administered to treat diseases associated with aberrant Blys expression  
XX and activity such as cancer, immune, and autoimmune disorders and  
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
XX the antibodies and fragments of the antibodies described in the method of  
XX the invention  
XX  
XX Sequence 249 AA;  
SQ  
Query Match 100.0%; Score 585; DB 5; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1e-36;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AFSSSETLDPANVVALGQTVRVTCQDLSRSYASWYQKPGQAPLVLYGKNNRSGIP 60  
DB 139 AFSSSETLDPANVVALGQTVRVTCQDLSRSYASWYQKPGQAPLVLYGKNNRSGIP 198  
QY 61 DRFGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFGGTETLVLG 111  
DB 199 DRFGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFGGTETLVLG 249

RESULT 9  
ABP44432 standard; protein; 249 AA.  
XX AC ABP44432;  
XX AC  
XX 19-AUG-2002 (first entry)  
XX DT  
XX DE Human Blys binding scFv SEQ ID 443.  
XX KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX KW tumor necrosis factor; B cell proliferation; B cell differentiation;  
XX KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
OS Homo sapiens.  
WO200202641-A1.  
XX PD 10-JAN-2002.  
XX PF 15-JUN-2001; 2001WO-US019110.  
XX PR 16-JUN-2000; 2000US-0212210P.  
XX PR 17-OCT-2000; 2000US-0240816P.  
XX PR 16-MAR-2001; 2001US-0276248P.  
XX PR 21-MAR-2001; 2001US-0277379P.  
XX PR 25-MAY-2001; 2001US-0293499P.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX PI WPI; 2002-114799/15.  
XX PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
XX PT diagnosis and treatment of cancers and immune disorders.  
XX PS Claim 1; Page 932-933; 3148pp; English.  
XX XX This invention describes novel antibodies that immunospecifically bind to  
XX CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
XX CC tumor necrosis factor (TNF) super family and induces B cell  
XX CC proliferation and differentiation. The antibodies of the invention have  
XX CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
XX CC antirheumatic and antiAIDS activity and can be used in vaccines to  
XX CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
XX CC and so may be used to detect and quantitate the presence of Blys in  
XX CC biological samples and may be used in this way to diagnose disease  
XX CC associated with aberrant expression of Blys. They may also be  
XX CC administered to treat diseases associated with aberrant Blys expression  
XX CC and activity such as cancer, immune, and autoimmune disorders and  
XX CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
XX CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
XX CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
XX CC the antibodies and fragments of the antibodies described in the method of  
XX CC the invention  
SQ Sequence 249 AA;  
Query Match 100.0%; Score 585; DB 5; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1e-36;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 199 DRFGSSSGNTSLTITGAQAEADYYCNSRDSGNHWFGGTELTVLG 249  
RESULT 10  
ABP44451  
XX ID ABP44451 standard; protein; 249 AA.  
XX AC ABP44451;  
XX AC  
XX 19-AUG-2002 (first entry)  
XX DT  
XX DE Human Blys binding scFv SEQ ID 462.  
XX KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX KW tumor necrosis factor; B cell proliferation; B cell differentiation;  
XX KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
OS Homo sapiens.  
WO200202641-A1.  
XX PD 10-JAN-2002.  
XX PF 15-JUN-2001; 2001WO-US019110.  
XX PR 16-JUN-2000; 2000US-0212210P.  
XX PR 17-OCT-2000; 2000US-0240816P.  
XX PR 16-MAR-2001; 2001US-0276248P.  
XX PR 21-MAR-2001; 2001US-0277379P.  
XX PR 25-MAY-2001; 2001US-0293499P.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX PI WPI; 2002-114799/15.  
XX PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
XX PT diagnosis and treatment of cancers and immune disorders.  
XX PS Claim 1; Page 954-955; 3148pp; English.  
XX XX This invention describes novel antibodies that immunospecifically bind to  
XX CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
XX CC tumor necrosis factor (TNF) super family and induces B cell  
XX CC proliferation and differentiation. The antibodies of the invention have  
XX CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
XX CC antirheumatic and antiAIDS activity and can be used in vaccines to  
XX CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
XX CC and so may be used to detect and quantitate the presence of Blys in  
XX CC biological samples and may be used in this way to diagnose disease  
XX CC associated with aberrant expression of Blys. They may also be  
XX CC administered to treat diseases associated with aberrant Blys expression  
XX CC and activity such as cancer, immune, and autoimmune disorders and  
XX CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
XX CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
XX CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
XX CC the antibodies and fragments of the antibodies described in the method of  
XX CC the invention  
SQ Sequence 249 AA;  
Query Match 100.0%; Score 585; DB 5; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1e-36;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 139 AFSSSELTDPAYVALGQTVRVTCQGDLSRSYYASWYQOKPGQAPVLVTYIGKNNRPSGIP 198  
QY 61 DRFGSSSGNTASLTITGAQAEADYCNRSRDSGNHWYFGGTELTVLG 111  
DB 199 DRFGSSSGNTASLTITGAQAEADYCNRSRDSGNHWYFGGTELTVLG 249

RESULT 11  
ABP44477  
ID ABP44477 standard; protein; 249 AA.  
AC ABP44477;  
XX  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scFv SEQ ID 488.  
XX  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
OS Homo sapiens.  
XX  
XX WO200202641-A1.  
XX  
XX 10-JAN-2002.  
XX  
XX 15-JUN-2001; 2001WO-US019110.  
XX  
XX 16-JUN-2000; 2000US-0212210P.  
XX 17-OCT-2000; 2000US-0240816P.  
XX 16-MAR-2001; 2001US-0276248P.  
XX 21-MAR-2001; 2001US-0277379P.  
XX 25-MAY-2001; 2001US-0293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
XX diagnosis and treatment of cancers and immune disorders.  
XX  
XX Claim 1; Page 985-986; 3148pp; English.

This invention describes novel antibodies that immunospecifically bind to B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of Blys. The antibodies bind to Blys and so may be used to detect and quantitate the presence of Blys in biological samples and may be used in this way to diagnose disease associated with aberrant expression of Blys. They may also be administered to treat diseases associated with aberrant Blys expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention

Sequence 249 AA;  
SQ

Query Match 100.0%; Score 585; DB 5; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1e-36;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFSSSELTDPAYVALGQTVRVTCQGDLSRSYYASWYQOKPGQAPVLVTYIGKNNRPSGIP 60  
DB 139 AFSSSELTDPAYVALGQTVRVTCQGDLSRSYYASWYQOKPGQAPVLVTYIGKNNRPSGIP 198  
QY 61 DRFGSSSGNTASLTITGAQAEADYCNRSRDSGNHWYFGGTELTVLG 111  
DB 199 DRFGSSSGNTASLTITGAQAEADYCNRSRDSGNHWYFGGTELTVLG 249

RESULT 12  
ABP44497  
ID ABP44497 standard; protein; 249 AA.  
AC ABP44497;  
XX  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scFv SEQ ID 508.  
XX  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
OS Homo sapiens.  
XX  
XX WO200202641-A1.  
XX  
XX 10-JAN-2002.  
XX  
XX 15-JUN-2001; 2001WO-US019110.  
XX  
XX 16-JUN-2000; 2000US-0212210P.  
XX 17-OCT-2000; 2000US-0240816P.  
XX 16-MAR-2001; 2001US-0276248P.  
XX 21-MAR-2001; 2001US-0277379P.  
XX 25-MAY-2001; 2001US-0293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
XX diagnosis and treatment of cancers and immune disorders.  
XX  
XX Claim 1; Page 1009-1010; 3148pp; English.

This invention describes novel antibodies that immunospecifically bind to B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of Blys. The antibodies bind to Blys and so may be used to detect and quantitate the presence of Blys in biological samples and may be used in this way to diagnose disease associated with aberrant expression of Blys. They may also be administered to treat diseases associated with aberrant Blys expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention

Sequence 249 AA;  
SQ

Query Match 100.0%; Score 585; DB 5; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1e-36;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFSSSLTQDPAVSVALGQTVRTCCGDSLRSYASWYQKRGQAPVLYIYGNRRPSGIP 60  
DB 139 AFSSSLTQDPAVSVALGQTVRTCCGDSLRSYASWYQKRGQAPVLYIYGNRRPSGIP 198

QY 61 DRFGSSSGNTASLTITGAQAEDEADYCNRRSSGNHWFGGTELTVLG 111  
DB 199 DRFGSSSGNTASLTITGAQAEDEADYCNRRSSGNHWFGGTELTVLG 249

RESULT 13  
ABP44548  
ID ABP44548 standard; protein; 249 AA.  
AC ABP44548;  
XX 19-AUG-2002 (first entry)

XX Human Blys binding scFv SEQ ID 559.  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX Homo sapiens.  
XX WO200202641-A1.  
XX 10-JAN-2002.  
XX 15-JUN-2001; 2001WO-US019110.  
XX 16-JUN-2000; 2000US-0212210P.  
XX 17-OCT-2000; 2000US-0240816P.  
XX 16-MAR-2001; 2001US-0276248P.  
XX 21-MAR-2001; 2001US-0277379P.  
XX 25-MAY-2001; 2001US-0293499P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.

XX Antibodies against B lymphocyte stimulating polypeptides, useful for the  
XX diagnosis and treatment of cancers and immune disorders.  
XX Claim 1; Page 1069-1070; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to  
XX B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
XX tumour necrosis factor (TNF) super family and induces B cell  
XX proliferation and differentiation. The antibodies of the invention have  
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
XX antirheumatic and antiAIDS activity and can be used in vaccines to  
XX inhibit the expression and activity of Blys. The antibodies bind to Blys  
XX and so may be used to detect and quantitate the presence of Blys in  
XX biological samples and may be used in this way to diagnose disease  
XX associated with aberrant expression of Blys. They may also be  
XX administered to treat diseases associated with aberrant Blys expression  
XX and activity such as cancer, immune, and autoimmune disorders and  
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
XX the antibodies and fragments of the antibodies described in the method of  
XX the invention

XX Sequence 249 AA;  
SQ Query Match 100.0%; Score 585; DB 5; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1e-36;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFSSSLTQDPAVSVALGQTVRTCCGDSLRSYASWYQKRGQAPVLYIYGNRRPSGIP 60  
DB 139 AFSSSLTQDPAVSVALGQTVRTCCGDSLRSYASWYQKRGQAPVLYIYGNRRPSGIP 198

QY 61 DRFGSSSGNTASLTITGAQAEDEADYCNRRSSGNHWFGGTELTVLG 111  
DB 199 DRFGSSSGNTASLTITGAQAEDEADYCNRRSSGNHWFGGTELTVLG 249

RESULT 14  
ABP44613  
ID ABP44613 standard; protein; 249 AA.  
AC ABP44613;  
XX 19-AUG-2002 (first entry)

XX Human Blys binding scFv SEQ ID 624.  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX Homo sapiens.  
XX WO200202641-A1.  
XX 10-JAN-2002.  
XX 15-JUN-2001; 2001WO-US019110.  
XX 16-JUN-2000; 2000US-0212210P.  
XX 17-OCT-2000; 2000US-0240816P.  
XX 16-MAR-2001; 2001US-0276248P.  
XX 21-MAR-2001; 2001US-0277379P.  
XX 25-MAY-2001; 2001US-0293499P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.

XX Antibodies against B lymphocyte stimulating polypeptides, useful for the  
XX diagnosis and treatment of cancers and immune disorders.  
XX Claim 1; Page 1146-1147; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to  
XX B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
XX tumour necrosis factor (TNF) super family and induces B cell  
XX proliferation and differentiation. The antibodies of the invention have  
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
XX antirheumatic and antiAIDS activity and can be used in vaccines to  
XX inhibit the expression and activity of Blys. The antibodies bind to Blys  
XX and so may be used to detect and quantitate the presence of Blys in  
XX biological samples and may be used in this way to diagnose disease  
XX associated with aberrant expression of Blys. They may also be  
XX administered to treat diseases associated with aberrant Blys expression  
XX and activity such as cancer, immune, and autoimmune disorders and  
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and

CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention

XX Sequence 249 AA;

Query Match 100.0%; Score 585; DB 5; Length 249;

Best Local Similarity 100.0%; Pred. No. 1e-36; Mismatches 0; Indels 0; Gaps 0;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFSSELTODPAVSVALGQTVRVTCQSDLSRSYASWYQOKPGQAPVLVIYGNRRPSGIP 60

DB 139 AFSSELTODPAVSVALGQTVRVTCQSDLSRSYASWYQOKPGQAPVLVIYGNRRPSGIP 198

QY 61 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWVFGGTELTVLG 111

DB 199 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWVFGGTELTVLG 249

LT 15

ID 4621 ABP4621 standard; protein; 249 AA.

AC ABP4621;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 632.

KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;

KW tumour necrosis factor; B cell proliferation; B cell differentiation;

KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

PI WPI; 2002-114799/15.

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the

PT diagnosis and treatment of cancers and immune disorders.

XX Claim 1; Page 1156-1157; 3148pp; English.

CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention

XX Sequence 249 AA;

Query Match 100.0%; Score 585; DB 5; Length 249;

Best Local Similarity 100.0%; Pred. No. 1e-36; Mismatches 0; Indels 0; Gaps 0;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFSSELTODPAVSVALGQTVRVTCQSDLSRSYASWYQOKPGQAPVLVIYGNRRPSGIP 60

DB 139 AFSSELTODPAVSVALGQTVRVTCQSDLSRSYASWYQOKPGQAPVLVIYGNRRPSGIP 198

QY 61 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWVFGGTELTVLG 111

DB 199 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWVFGGTELTVLG 249

Search completed: September 9, 2004, 11:06:31  
Job time : 48.9103 secs

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## OM protein - protein search, using sw model

Run on: September 9, 2004, 11:04:55 ; Search time 14.2308 Seconds  
(without alignments)  
402.683 Million cell updates/sec

Title: US-09-880-748-2\_COPY\_139\_249

Perfect score: 585  
Sequence: 1 AFSSSLTQDPNPAVALGQTV.....RDSGNHWFGGTELTIVLG 111

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 70 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/2/1aa/5A COMB. pep:\*
- 2: /cgn2\_6/prodata/2/1aa/5B COMB. pep:\*
- 3: /cgn2\_6/prodata/2/1aa/6A COMB. pep:\*
- 4: /cgn2\_6/prodata/2/1aa/6B COMB. pep:\*
- 5: /cgn2\_6/prodata/2/1aa/6C COMB. pep:\*
- 6: /cgn2\_6/prodata/2/1aa/6D COMB. pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	95.0	278	3	US-09-260-527-3
2	556	95.0	280	4	US-09-260-527-1
3	556	95.0	309	4	US-09-079-029-9
4	556	95.0	312	2	US-09-079-029-10
5	540.5	92.4	109	2	US-08-665-202-34
6	540.5	92.4	109	4	US-09-115-574-34
7	529	90.4	109	2	US-08-652-816A-16
8	494	84.4	97	2	US-08-665-202-35
9	494	84.4	97	4	US-09-315-574-35
10	489.5	83.7	104	4	US-08-793-450-2
11	489.5	83.7	238	4	US-08-793-450-6
12	475	81.2	104	3	US-09-240-274-49
13	468	80.0	106	3	US-09-240-274-48
14	468	80.0	106	3	US-09-240-274-50
15	463	79.1	103	2	US-08-273-146-71
16	461	78.8	106	3	US-09-240-274-47
17	436.5	74.6	108	4	US-09-025-769B-20
18	431.5	73.8	105	1	US-08-488-113B-157
19	431.5	73.8	105	1	US-08-477-484B-157
20	431.5	73.8	105	1	US-08-107-669D-21
21	431.5	73.8	105	1	US-08-472-788A-21
22	431.5	73.8	105	2	US-08-477-531B-21
23	431.5	73.8	105	2	US-08-646-360-157
24	431.5	73.8	105	2	US-08-082-842A-21
25	431.5	73.8	105	3	US-08-839-765-157
26	431.5	73.8	105	3	US-09-136-389-157
27	431.5	73.8	105	4	US-09-610-838-157

## ALIGNMENTS

28	431.5	73.8	105	4	US-09-711-485-157	Sequence 157, App
29	417	71.3	108	1	US-08-360-125-12	Sequence 12, Appl
30	417	71.3	108	2	US-08-450-578-12	Sequence 12, Appl
31	417	71.3	108	2	US-09-017-628-12	Sequence 12, Appl
32	417	71.3	108	2	US-09-014-880-12	Sequence 12, Appl
33	417	71.3	108	4	US-08-450-363-12	Sequence 12, Appl
34	407	69.6	109	3	US-09-157-370-5	Sequence 5, Appl
35	395	67.5	107	4	US-09-025-769B-34	Sequence 34, Appl
36	395	67.5	107	4	US-09-025-769B-55	Sequence 55, Appl
37	391.5	66.9	249	4	US-10-039-785-53	Sequence 53, Appl
38	385	65.8	109	1	US-08-478-039-91	Sequence 91, Appl
39	385	65.8	109	1	US-08-476-349A-91	Sequence 91, Appl
40	381.5	65.2	143	2	US-08-345-321-8	Sequence 8, Appl
41	379	64.8	108	1	US-08-259-372A-10	Sequence 10, Appl
42	379	64.8	108	1	US-08-468-671-10	Sequence 10, Appl
43	379	64.8	234	3	US-08-487-550-2	Sequence 2, Appl
44	379	64.8	234	4	US-09-526-098-2	Sequence 2, Appl
45	370	63.2	106	1	US-08-259-372A-16	Sequence 16, Appl
46	370	63.2	106	1	US-08-468-671-16	Sequence 16, Appl
47	369	63.1	128	1	US-08-478-039-110	Sequence 110, App
48	369	63.1	128	1	US-08-476-349A-110	Sequence 110, App
49	369	63.1	128	3	US-08-523-894-4	Sequence 4, Appl
50	369	63.1	233	3	US-08-523-894-6	Sequence 6, Appl
51	364	62.2	245	4	US-10-039-785-42	Sequence 42, Appl
52	362	61.9	109	1	US-08-478-039-92	Sequence 92, Appl
53	362	61.9	109	1	US-08-476-349A-92	Sequence 92, Appl
54	355	60.7	109	3	US-09-202-181-2	Sequence 2, Appl
55	353.5	60.4	112	2	US-08-665-202-39	Sequence 39, Appl
56	353.5	60.4	112	4	US-09-315-574-39	Sequence 39, Appl
57	353	60.3	111	2	US-08-665-202-36	Sequence 36, Appl
58	353	60.3	111	4	US-09-315-574-36	Sequence 36, Appl
59	353	60.3	258	2	US-08-665-202-5	Sequence 5, Appl
60	353	60.3	258	4	US-09-315-574-5	Sequence 5, Appl
61	353	60.3	262	4	US-09-069-821-4	Sequence 4, Appl
62	353	60.3	282	4	US-09-420-592A-7	Sequence 7, Appl
63	351.5	60.1	236	3	US-09-049-672A-7	Sequence 7, Appl
64	349.5	59.7	103	3	US-09-240-274-66	Sequence 66, Appl
65	349.5	59.7	110	3	US-09-240-274-63	Sequence 63, Appl
66	348	59.5	111	2	US-08-665-202-40	Sequence 40, Appl
67	348	59.5	111	4	US-09-315-574-40	Sequence 40, Appl
68	347	59.3	111	2	US-08-665-202-43	Sequence 43, Appl
69	347	59.3	111	4	US-09-315-574-43	Sequence 43, Appl
70	347	59.3	245	4	US-10-039-785-48	Sequence 48, Appl

RESULT 1  
US-09-260-527-3  
Sequence 3, Application US/09260527A  
Patent No. 6228599  
GENERAL INFORMATION:  
APPLICANT: Knox, J.P.  
APPLICANT: Mikkelson, J.D.  
APPLICANT: Mikkelson, W.G.  
TITLE OF INVENTION: ANTIBODY  
FILE REFERENCE: DYOUI9, 001AUS  
CURRENT APPLICATION NUMBER: US/09/260,527A  
CURRENT FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 278  
TYPE: PRT  
ORGANISM: UNKNOWN  
FEATURE:  
OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected from a naive phage display library known as the  
OTHER INFORMATION: Synthetic scfv library (#1) from the Centre for  
OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK  
US-09-260-527-3

Query Match 95.0%; Score 556; DB 3; Length 278;  
Best Local Similarity 97.2%; Pred. No. 1.3e-45;  
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SSELTPDPAVSVALGQTVRTTCGDSLSRSYASWYQKPGQAPVLYVIGKNNRPSGIPDR 62  
DB 153 SSELTPDPAVSVALGQTVRTTCGDSLSRSYASWYQKPGQAPVLYVIGKNNRPSGIPDR 212

QY 63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWFGGTELTVLG 111  
DB 213 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWFGGTELTVLG 261

RESULT 2  
US-09-260-527-1  
Sequence 1, Application US/09260527A  
Patent No. 6228599  
GENERAL INFORMATION:

APPLICANT: Knox, J.P.  
APPLICANT: Mikkelson, J.D.  
APPLICANT: Wallats, W. G.

TITLE OF INVENTION: ANTIBODY  
FILE REFERENCE: DYOUL9.001AUS  
CURRENT APPLICATION NUMBER: US/09/260,527A  
CURRENT FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FaalSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 280  
TYPE: PRT  
ORGANISM: UNKNOWN

FEATURE:  
OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a  
OTHER INFORMATION: phage display library known as the Synthetic scfv  
OTHER INFORMATION: Library (#1) from the Centre for Protein  
OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.  
US-09-260-527-1

Query Match 95.0%; Score 556; DB 3; Length 280;  
Best Local Similarity 97.2%; Pred. No. 1.3e-45;  
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SSELTPDPAVSVALGQTVRTTCGDSLSRSYASWYQKPGQAPVLYVIGKNNRPSGIPDR 62  
DB 155 SSELTPDPAVSVALGQTVRTTCGDSLSRSYASWYQKPGQAPVLYVIGKNNRPSGIPDR 214

QY 63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWFGGTELTVLG 111  
215 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWFGGTELTVLG 263

RESULT 3  
US-09-079-029-9  
Sequence 9, Application US/09079029  
Patent No. 6342369  
GENERAL INFORMATION:

APPLICANT: Adams, Camilla W.  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Chuntharapal, Anan  
APPLICANT: Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,029  
FILING DATE:

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-079-029-9

Query Match 95.0%; Score 556; DB 4; Length 309;  
Best Local Similarity 97.2%; Pred. No. 1.5e-45;  
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SSELTPDPAVSVALGQTVRTTCGDSLSRSYASWYQKPGQAPVLYVIGKNNRPSGIPDR 62  
DB 175 SSELTPDPAVSVALGQTVRTTCGDSLSRSYASWYQKPGQAPVLYVIGKNNRPSGIPDR 234

QY 63 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWFGGTELTVLG 111  
DB 235 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWFGGTELTVLG 283

RESULT 4  
US-09-079-029-10  
Sequence 10, Application US/09079029  
Patent No. 6342369  
GENERAL INFORMATION:

APPLICANT: Adams, Camilla W.  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Chuntharapal, Anan  
APPLICANT: Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,029  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 312 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-079-029-10

Query Match 95.0%; Score 556; DB 4; Length 312;  
Best Local Similarity 97.2%; Pred. No. 1.5e-45;  
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SSELTDPAVSVAGQTVRTCCGDSLRSYASWYQKPGQAPVLYIGKNNRPSGIPDR 62  
DB 178 SSELTDPAVSVAGQTVRTCCGDSLRSYASWYQKPGQAPVLYIGKNNRPSGIPDR 237

QY 63 FSGSSGNFASLTITGAQAEADYCNRSRDSGNHVFSGGTETVLG 111  
DB 238 FSGSSGNFASLTITGAQAEADYCNRSRDSGNHVFSGGTETVLG 286

## RESULT 5

US-08-665-202-34  
Sequence 34, Application US/08665202

Patent No. 5977322

GENERAL INFORMATION:

APPLICANT: Marks, James D.

APPLICANT: Schier, Robert

TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to

TUMOR ANTIGENS

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/665,202

FILING DATE: 13-JUN-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,238

FILING DATE: 14-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,250

FILING DATE: 15-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498

REFERENCE/DOCKET NUMBER: 02307E-061410

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-665-202-34

Query Match 92.4%; Score 540.5; DB 2; Length 109;

Best Local Similarity 94.5%; Pred. No. 1.3e-44;

Matches 103; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 4 SSELTDPAVSVAGQTVRTCCGDSLRSYASWYQKPGQAPVLYIGKNNRPSGIPDR 63

DB 1 SSELTDPAVSVAGQTVRTCCGDSLRSYASWYQKPGQAPVLYIGKNNRPSGIPDR 60

QY 64 SSSSSGNFASLTITGAQAEADYCNRSRDSGN-HWVFGGTETVLG 111

DB 61 SSSSSGNFASLTITGAQAEADYCNRSRDSGNHWVFGGTETVLG 109

RESULT 6  
US-09-315-574-34  
Sequence 34, Application US/09315574

Patent No. 6512097

GENERAL INFORMATION:

APPLICANT: Marks, James D.

APPLICANT: Schier, Robert

TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to

TUMOR ANTIGENS

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESSEE: Majestic, Parsons, Siebert & Hane P.C.

STREET: Four Embarcadero Center, Suite 1100

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-4106

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/315,574

FILING DATE: 20-MAY-99

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,238

FILING DATE: 14-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,250

FILING DATE: 15-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/665,202

FILING DATE: 13-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498

REFERENCE/DOCKET NUMBER: 02307E-061411

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-315-574-34

Query Match 92.4%; Score 540.5; DB 4; Length 109;

Best Local Similarity 94.5%; Pred. No. 1.3e-44;

Matches 103; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 4 SSELTDPAVSVAGQTVRTCCGDSLRSYASWYQKPGQAPVLYIGKNNRPSGIPDR 63

DB 1 SSELTDPAVSVAGQTVRTCCGDSLRSYASWYQKPGQAPVLYIGKNNRPSGIPDR 60

QY 64 SSSSSGNFASLTITGAQAEADYCNRSRDSGN-HWVFGGTETVLG 111

DB 61 SSSSSGNFASLTITGAQAEADYCNRSRDSGNHWVFGGTETVLG 109

## RESULT 7

US-08-652-816A-16  
Sequence 16, Application US/08652816A

Patent No. 5872215

GENERAL INFORMATION:

APPLICANT: Osbourn, JK

APPLICANT: Allen, DJ

APPLICANT: McCafferty, JG

TITLE OF INVENTION: Specific binding members, materials and  
TITLE OF INVENTION: methods.  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,816A  
FILING DATE: 23-MAY-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.4  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.8  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 23-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9525004.9  
FILING DATE: 07-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9610824.6  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/02240  
FILING DATE: 02-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/244,597  
FILING DATE: 01-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/33308  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-652-816A-16

Query Match 90.4%; Score 529; DB 2; Length 109;  
Best Local Similarity 93.5%; Pred. No. 1.7e-43;  
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 SSELDDPAVSVALGQTVAVTCQGSLSRSYASWYQKRGQAPVLYIGKNNRPSGIDPR 62  
DB 1 SSELDDPAVSVALGQTVAVTCQGSLSRSYASWYQKRGQAPVLYIGKNNRPSGIDPR 60

QY 63 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVVFGGGLTLEI 109  
DB 61 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVVFGGGLTLEI 107

RESULT 8  
US-08-665-202-35  
Sequence 35, Application US/08665202  
Patent No. 5977322  
GENERAL INFORMATION:  
APPLICANT: Marks, James D.

APPLICANT: Schier, Robert  
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to  
TITLE OF INVENTION: Tumor Antigens  
NUMBER OF SEQUENCES: 141  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/665,202  
FILING DATE: 13-JUN-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,238  
FILING DATE: 14-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,250  
FILING DATE: 15-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 02307E-061410  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 97 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-665-202-35

Query Match 84.4%; Score 494; DB 2; Length 97;  
Best Local Similarity 96.9%; Pred. No. 3.2e-40;  
Matches 94; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 SSELDDPAVSVALGQTVAVTCQGSLSRSYASWYQKRGQAPVLYIGKNNRPSGIDPR 63  
DB 1 SSELDDPAVSVALGQTVAVTCQGSLSRSYASWYQKRGQAPVLYIGKNNRPSGIDPR 60

QY 64 SSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVV 100  
DB 61 SSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVV 97

RESULT 9  
US-09-315-574-35  
Sequence 35, Application US/09315574  
Patent No. 6512097  
GENERAL INFORMATION:  
APPLICANT: Marks, James D.  
TITLE OF INVENTION:  
ADDRESSEE: Schier, Robert  
TITLE OF INVENTION: No. 6512097e1 High Affinity Human Antibodies to  
TITLE OF INVENTION: Tumor Antigens  
NUMBER OF SEQUENCES: 141  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.  
STREET: Four Embarcadero Center, Suite 1100  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4106  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/315,574  
FILING DATE: 20-MAY-99  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,238  
FILING DATE: 14-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,250  
FILING DATE: 15-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/665,202  
FILING DATE: 13-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 02307E-061411  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 97 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-315-574-35

Query Match 84.4%; Score 494; DB 4; Length 97;  
Best Local Similarity 96.9%; Pred. No. 3.2e-40;  
Matches 94; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 4 SEITOPAVSVALGQVTRVTCOGDSLRSYASWYQKPGAPVLVIYGNRRPSCIPDRF 63  
DB 1 SSILOPAVSVALGQVTRVTCOGDSLRSYASWYQKPGAPVLVIYGNRRPSCIPDRF 60  
QY 64 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHW 100  
DB 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHW 97

RESULT 10  
US-08-793-450-2  
Sequence 2, Application US/08793450  
Patent No. 6312690  
GENERAL INFORMATION:  
APPLICANT: EDELMAN, LENA  
APPLICANT: MARGARITTE, CHRISTEL  
APPLICANT: KACZOREK, MICHEL  
APPLICANT: CHABIBI, HASSAN  
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,450

FILING DATE: 03-MAR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 94/10566  
FILING DATE: 02-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-793-450-2

Query Match 83.7%; Score 489.5; DB 4; Length 104;  
Best Local Similarity 88.8%; Pred. No. 9.3e-40;  
Matches 95; Conservative 4; Mismatches 3; Indels 5; Gaps 1;  
QY 5 ELTODPAVSVALGQVTRVTCOGDSLRSYASWYQKPGAPVLVIYGNRRPSCIPDRF 64  
DB 3 SSILOPAVSVALGQVTRVTCOGDSLRSYASWYQKPGAPVLVIYGNRRPSCIPDRF 62  
QY 65 GSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWFGGTETLVIG 111  
DB 63 GSSSSGNTASLTITGAQAEDEADYYCNSGK-----VFGGTETLVIG 104

RESULT 11  
US-08-793-450-6  
Sequence 6, Application US/08793450  
Patent No. 6312690  
GENERAL INFORMATION:  
APPLICANT: EDELMAN, LENA  
APPLICANT: MARGARITTE, CHRISTEL  
APPLICANT: KACZOREK, MICHEL  
APPLICANT: CHABIBI, HASSAN  
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,450  
FILING DATE: 03-MAR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 94/10566  
FILING DATE: 02-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 238 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-793-450-6

Query Match 83.7%; Score 489.5; DB 4; Length 238;  
Best Local Similarity 88.8%; Pred. No. 2.4e-39;  
Matches 95; Conservative 4; Mismatches 3; Indels 5; Gaps 1;

QY 5 ELTOPAVSVALGQTVRTTCGDSLSRSYYASWYQKPGQAPLVYIGKNNRPSGIPDRSGSS 64  
DB 22 ELTOPAVSVALGQTVRTTCGDSLSRSYYASWYQKPGQAPLVYIGKNNRPSGIPDRSGSS 81

QY 65 GSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWFGGTELTIVL 111  
DB 82 GSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWFGGTELTIVL 123

LT 12  
US-09-240-274-49  
Sequence 49, Application US/09240274  
Patent No. 6255455

GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/240,274  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 49  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain J04  
US-09-240-274-49

Query Match 81.2%; Score 475; DB 3; Length 104;  
Best Local Similarity 89.3%; Pred. No. 2.3e-38;  
Matches 92; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 8 QDPVAVSVALGQTVRTTCGDSLSRSYYASWYQKPGQAPLVYIGKNNRPSGIPDRSGSS 67  
DB 4 QDPVAVSVALGQTVRTTCGDSLSRSYYASWYQKPGQAPLVYIGKNNRPSGIPDRSGSS 63

QY 68 SGTASLTITGAQAEDEADYYCNSRDSGNNHWFGGTELTIVL 110  
DB 64 SGTASLTITGAQAEDEADYYCNSRDSGNNHWFGGTELTIVL 104

RESULT 13  
US-09-240-274-48  
Sequence 48, Application US/09240274  
Patent No. 6255455

GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/240,274  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 48  
LENGTH: 106  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain J02  
US-09-240-274-48

Query Match 80.0%; Score 468; DB 3; Length 106;  
Best Local Similarity 85.4%; Pred. No. 1.1e-37;  
Matches 88; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 8 QDPVAVSVALGQTVRTTCGDSLSRSYYASWYQKPGQAPLVYIGKNNRPSGIPDRSGSS 67  
DB 4 QDPVAVSVALGQTVRTTCGDSLSRSYYASWYQKPGQAPLVYIGKNNRPSGIPDRSGSS 63

QY 68 SGTASLTITGAQAEDEADYYCNSRDSGNNHWFGGTELTIVL 110  
DB 64 SGTASLTITGAQAEDEADYYCNSRDSGNNHWFGGTELTIVL 106

RESULT 14  
US-09-240-274-50  
Sequence 50, Application US/09240274  
Patent No. 6255455

GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/240,274  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 50  
LENGTH: 106  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain J05  
US-09-240-274-50

Query Match 80.0%; Score 468; DB 3; Length 106;  
Best Local Similarity 83.5%; Pred. No. 1.1e-37;  
Matches 86; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 8 QDPVAVSVALGQTVRTTCGDSLSRSYYASWYQKPGQAPLVYIGKNNRPSGIPDRSGSS 67  
DB 4 QDPVAVSVALGQTVRTTCGDSLSRSYYASWYQKPGQAPLVYIGKNNRPSGIPDRSGSS 63

QY 68 SGTASLTITGAQAEDEADYYCNSRDSGNNHWFGGTELTIVL 110  
DB 64 SGTASLTITGAQAEDEADYYCNSRDSGNNHWFGGTELTIVL 106

RESULT 15  
US-08-273-146-71  
Sequence 71, Application US/08273146  
Patent No. 5855885

GENERAL INFORMATION:  
APPLICANT: Smith, Roger  
APPLICANT: McCafferty, John  
APPLICANT: Chiswell, David  
APPLICANT: Datsley, Michael J.  
APPLICANT: Fitzgerald, Kevin  
APPLICANT: Kenten, John H.  
APPLICANT: Martin, Mark T.

APPLICANT: Titmas, Richard C.  
APPLICANT: Williams, Richard O.  
TITLE OF INVENTION: The Isolation and Production of  
TITLE OF INVENTION: Catalytic Antibodies using Phage Technology  
NUMBER OF SEQUENCES: 71  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: IGEN, Inc.  
STREET: 1530 East Jefferson St.  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20852  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/273,146  
FILING DATE: 14-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ryan, John W.  
REGISTRATION NUMBER: 33,771  
REFERENCE/DOCKET NUMBER: 09000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-984-8000  
TELEFAX: 301-230-0158  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 103 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-273-146-71

Query Match 79.1%; Score 463; DB 2; Length 103;  
Best Local Similarity 90.8%; Pred. No. 3.1e-37;  
Matches 89; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
QY 14 VALGQTVRYVTCQGDLSRYYASWYQOKPGQAPVLYIGKNNRPSGIPDRFSGSSSGNTAS 73  
DB 6 VALGQTVRYVTCQGDLSRYYASWYQOKPGQAPVLYIGKNNRPSGIPDRFSGSSSGNTAS 65  
QY 74 LTTTGAQAEDEADYYCNSRDSGSHWVFGGGLTVLG 111  
DB 66 LTTTGAQAEDEADYYCNSRDSGSHWVFGGGLTVLG 103

Search completed: September 9, 2004, 11:09:20  
Job time: 16.2308 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 9, 2004, 11:07:30 ; Search time 81.5897 Seconds  
(without alignments)  
436.287 Million cell updates/sec

Title: US-09-880-748-2\_COPY\_139\_249

Perfect score: 585  
Sequence: 1 ARSSELTPQPAVVALGQTV.....RDSGNHWVFGGTELTVLG 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

1 number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 70 summaries

Database :

Published Applications AA:\*

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18: /cgn2\_6/ptodata/2/pubppa/US06\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	585	100.0	248	10	US-09-880-748-339 Sequence 339, App
2	585	100.0	248	10	US-09-880-748-347 Sequence 347, App
3	585	100.0	248	10	US-09-880-748-354 Sequence 354, App
4	585	100.0	248	10	US-09-880-748-357 Sequence 357, App
5	585	100.0	248	10	US-09-880-748-623 Sequence 623, App
6	585	100.0	248	10	US-09-880-748-633 Sequence 633, App
7	585	100.0	248	10	US-09-880-748-347 Sequence 347, App
8	585	100.0	248	10	US-09-880-748-354 Sequence 354, App
9	585	100.0	248	10	US-09-880-748-357 Sequence 357, App
10	585	100.0	248	10	US-09-880-748-623 Sequence 623, App
11	585	100.0	249	10	US-09-880-748-347 Sequence 347, App
12	585	100.0	249	10	US-09-880-748-354 Sequence 354, App
13	585	100.0	249	10	US-09-880-748-357 Sequence 357, App
14	585	100.0	249	10	US-09-880-748-623 Sequence 623, App
15	585	100.0	249	10	US-09-880-748-633 Sequence 633, App

16	585	100.0	249	10	US-09-880-748-333 Sequence 333, App
17	585	100.0	249	10	US-09-880-748-347 Sequence 347, App
18	585	100.0	249	10	US-09-880-748-354 Sequence 354, App
19	585	100.0	249	10	US-09-880-748-357 Sequence 357, App
20	585	100.0	249	10	US-09-880-748-623 Sequence 623, App
21	585	100.0	249	10	US-09-880-748-633 Sequence 633, App
22	585	100.0	249	10	US-09-880-748-347 Sequence 347, App
23	585	100.0	249	10	US-09-880-748-354 Sequence 354, App
24	585	100.0	249	10	US-09-880-748-357 Sequence 357, App
25	585	100.0	249	10	US-09-880-748-623 Sequence 623, App
26	585	100.0	249	10	US-09-880-748-633 Sequence 633, App
27	585	100.0	249	10	US-09-880-748-347 Sequence 347, App
28	585	100.0	249	10	US-09-880-748-354 Sequence 354, App
29	585	100.0	249	10	US-09-880-748-357 Sequence 357, App
30	585	100.0	249	10	US-09-880-748-623 Sequence 623, App
31	585	100.0	249	10	US-09-880-748-633 Sequence 633, App
32	585	100.0	249	10	US-09-880-748-347 Sequence 347, App
33	585	100.0	249	10	US-09-880-748-354 Sequence 354, App
34	585	100.0	249	10	US-09-880-748-357 Sequence 357, App
35	585	100.0	249	10	US-09-880-748-623 Sequence 623, App
36	585	100.0	249	10	US-09-880-748-633 Sequence 633, App
37	585	100.0	249	10	US-09-880-748-347 Sequence 347, App
38	585	100.0	249	10	US-09-880-748-354 Sequence 354, App
39	585	100.0	249	10	US-09-880-748-357 Sequence 357, App
40	585	100.0	249	10	US-09-880-748-623 Sequence 623, App
41	585	100.0	249	10	US-09-880-748-633 Sequence 633, App
42	585	100.0	249	10	US-09-880-748-347 Sequence 347, App
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44	585	100.0	249	10	US-09-880-748-357 Sequence 357, App
45	585	100.0	249	10	US-09-880-748-623 Sequence 623, App
46	585	100.0	249	10	US-09-880-748-633 Sequence 633, App
47	585	100.0	249	10	US-09-880-748-347 Sequence 347, App
48	585	100.0	249	10	US-09-880-748-354 Sequence 354, App
49	585	100.0	249	10	US-09-880-748-357 Sequence 357, App
50	585	100.0	249	10	US-09-880-748-623 Sequence 623, App
51	585	100.0	249	10	US-09-880-748-633 Sequence 633, App
52	585	100.0	249	10	US-09-880-748-347 Sequence 347, App
53	585	100.0	249	10	US-09-880-748-354 Sequence 354, App
54	585	100.0	249	10	US-09-880-748-357 Sequence 357, App
55	585	100.0	249	10	US-09-880-748-623 Sequence 623, App
56	585	100.0	249	10	US-09-880-748-633 Sequence 633, App
57	585	100.0	249	10	US-09-880-748-347 Sequence 347, App
58	585	100.0	249	10	US-09-880-748-354 Sequence 354, App
59	585	100.0	249	10	US-09-880-748-357 Sequence 357, App
60	585	100.0	249	10	US-09-880-748-623 Sequence 623, App
61	585	100.0	249	10	US-09-880-748-633 Sequence 633, App
62	585	100.0	249	10	US-09-880-748-347 Sequence 347, App
63	585	100.0	249	10	US-09-880-748-354 Sequence 354, App
64	585	100.0	249	10	US-09-880-748-357 Sequence 357, App
65	585	100.0	249	10	US-09-880-748-623 Sequence 623, App
66	585	100.0	249	10	US-09-880-748-633 Sequence 633, App
67	585	100.0	249	10	US-09-880-748-347 Sequence 347, App
68	585	100.0	249	10	US-09-880-748-354 Sequence 354, App
69	585	100.0	249	10	US-09-880-748-357 Sequence 357, App
70	585	100.0	249	10	US-09-880-748-623 Sequence 623, App

#### ALIGNMENTS

RESULT 1

US-09-880-748-339

Sequence 339, Application US/09880748

Publication No. US2003005937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

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; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 319
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-339

Query Match
Best Local Similarity 100.0%; Score 585; DB 10; Length 248;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AFSSSLTODPAVVALGQTVRVTCQGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIP 60
138 AFSSSLTODPAVVALGQTVRVTCQGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIP 197
61 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWFGGTELTVLG 111
198 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWFGGTELTVLG 248

RESULT 2
US-09-880-748-347
; Sequence 347, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 347
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-347

Query Match
Best Local Similarity 100.0%; Score 585; DB 10; Length 248;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AFSSSLTODPAVVALGQTVRVTCQGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIP 60
138 AFSSSLTODPAVVALGQTVRVTCQGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIP 197
61 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWFGGTELTVLG 111
198 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWFGGTELTVLG 248

RESULT 3
US-09-880-748-354
; Sequence 354, Application US/09880748
; Publication No. US20030059937A1
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; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 354
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-354
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Query Match
Best Local Similarity 100.0%; Score 585; DB 10; Length 248;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 AFSSSLTODPAVVALGQTVRVTCQGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIP 60
138 AFSSSLTODPAVVALGQTVRVTCQGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIP 197
61 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWFGGTELTVLG 111
198 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWFGGTELTVLG 248
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RESULT 4
US-09-880-748-597
; Sequence 597, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 597
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-597
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Query Match
Best Local Similarity 100.0%; Score 585; DB 10; Length 248;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 AFSSSLTODPAVVALGQTVRVTCQGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIP 60
138 AFSSSLTODPAVVALGQTVRVTCQGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIP 197
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; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 354
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-354

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Query Match          100.0%; Score 585; DB 12; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.7e-45;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AFSSSLTDDPAVSVALGQTVRVTCQGDLSRSYASWYQKPGQAPVLVIYGNRRPSGIP 60
DB 138 AFSSSLTDDPAVSVALGQTVRVTCQGDLSRSYASWYQKPGQAPVLVIYGNRRPSGIP 197
QY 61 DRFSGSSSGNTASLTITGAQAEADYDYYCNSRDSGNNHWVFGGTELTVLG 111
DB 198 DRFSGSSSGNTASLTITGAQAEADYDYYCNSRDSGNNHWVFGGTELTVLG 248

```

```

RESULT 9
US-10-293-418-597
; Sequence 597, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 597
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-597

```

```

Query Match          100.0%; Score 585; DB 12; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.7e-45;

```

```

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AFSSSLTDDPAVSVALGQTVRVTCQGDLSRSYASWYQKPGQAPVLVIYGNRRPSGIP 60
DB 138 AFSSSLTDDPAVSVALGQTVRVTCQGDLSRSYASWYQKPGQAPVLVIYGNRRPSGIP 197
QY 61 DRFSGSSSGNTASLTITGAQAEADYDYYCNSRDSGNNHWVFGGTELTVLG 111
DB 198 DRFSGSSSGNTASLTITGAQAEADYDYYCNSRDSGNNHWVFGGTELTVLG 248

```

```

RESULT 10
US-10-293-418-623
; Sequence 623, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 623
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-623

```

```

Query Match          100.0%; Score 585; DB 12; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.7e-45;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AFSSSLTDDPAVSVALGQTVRVTCQGDLSRSYASWYQKPGQAPVLVIYGNRRPSGIP 60
DB 138 AFSSSLTDDPAVSVALGQTVRVTCQGDLSRSYASWYQKPGQAPVLVIYGNRRPSGIP 197
QY 61 DRFSGSSSGNTASLTITGAQAEADYDYYCNSRDSGNNHWVFGGTELTVLG 111
DB 198 DRFSGSSSGNTASLTITGAQAEADYDYYCNSRDSGNNHWVFGGTELTVLG 248

```

```

RESULT 11
US-09-880-748-2
; Sequence 2, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16

```

PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 249  
TYPE: PRF  
ORGANISM: Homo sapiens  
US-09-880-748-2

Query Match 100.0%; Score 585; DB 10; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1.7e-45;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFSSSETDPAVVALGQTVRTCCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIP 60  
DB 139 AFSSSETDPAVVALGQTVRTCCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIP 198  
61 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTELTVLG 111  
199 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTELTVLG 249

## RESULT 12

US-09-880-748-323  
Sequence 323, Application US/09880748  
Publication No. US20030059937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PF523  
CURRENT APPLICATION NUMBER: US/09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 323  
LENGTH: 249  
TYPE: PRF  
ORGANISM: Homo sapiens  
US-09-880-748-323

Query Match 100.0%; Score 585; DB 10; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1.7e-45;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFSSSETDPAVVALGQTVRTCCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIP 60  
DB 139 AFSSSETDPAVVALGQTVRTCCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIP 198  
61 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTELTVLG 111  
199 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTELTVLG 249

## RESULT 13

US-09-880-748-324  
Sequence 324, Application US/09880748  
Publication No. US20030059937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 324  
LENGTH: 249  
TYPE: PRF  
ORGANISM: Homo sapiens  
US-09-880-748-324

Query Match 100.0%; Score 585; DB 10; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1.7e-45;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFSSSETDPAVVALGQTVRTCCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIP 60  
DB 139 AFSSSETDPAVVALGQTVRTCCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIP 198  
61 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTELTVLG 111  
199 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTELTVLG 249

## RESULT 14

US-09-880-748-326  
Sequence 326, Application US/09880748  
Publication No. US20030059937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PF523  
CURRENT APPLICATION NUMBER: US/09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 326  
LENGTH: 249  
TYPE: PRF  
ORGANISM: Homo sapiens  
US-09-880-748-326

Query Match 100.0%; Score 585; DB 10; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1.7e-45;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFSSSETDPAVVALGQTVRTCCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIP 60  
DB 139 AFSSSETDPAVVALGQTVRTCCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIP 198  
61 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTELTVLG 111  
199 DRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTELTVLG 249

RESULT 15

US-09-880-748-332  
 ; Sequence 332, Application US/09880748  
 ; Publication No. US20030059937A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
 ; FILE REFERENCE: PF523  
 ; CURRENT APPLICATION NUMBER: US/09/880,748  
 ; CURRENT FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: 60/212,210  
 ; PRIOR FILING DATE: 2000-06-15  
 ; PRIOR APPLICATION NUMBER: 60/240,816  
 ; PRIOR FILING DATE: 2000-10-17  
 ; PRIOR APPLICATION NUMBER: 60/276,248  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/277,379  
 ; PRIOR FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/293,499  
 ; PRIOR FILING DATE: 2001-05-25  
 ; NUMBER OF SEQ ID NOS: 3239  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 332  
 ; LENGTH: 249  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-880-748-332

Query Match 100.0%; Score 585; DB 10; Length 249;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-45;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AFSSELTDPAYVALGQTVRTVTCQSDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIP 60  
 DB 139 AFSSELTDPAYVALGQTVRTVTCQSDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIP 198  
 QY 61 DRPSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWFGGTELTVLG 111  
 DB 199 DRPSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHWFGGTELTVLG 249

Search completed: September 9, 2004, 11:23:43  
 Job time : 82.5897 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 9, 2004, 10:59:50 ; Search time 12.333 Seconds  
(without alignments)  
865.724 Million cell updates/sec

Title: US-09-880-748-2\_COPY\_139\_249

Perfect score: 585  
Sequence: 1 AFSSLETPDPAVVALQGVTV.....RDSGNHWVFGGTELTVLG 111

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 70 summaries

Database : PIR 78:\*

1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	95.0	109	2	S19663 Ig lambda chain V
2	550	94.0	108	2	S38498 Ig lambda chain -
3	550	94.0	108	2	S47184 Ig lambda chain -
4	544	93.0	127	2	S70444 Ig lambda chain pr
5	539.5	92.2	110	2	S36272 Ig lambda chain V
6	527	90.1	109	2	S38496 Ig lambda chain -
7	518	88.5	233	2	S25748 Ig lambda chain -
8	515	88.0	108	1	L3H0SH Ig lambda chain V-
9	510.5	87.3	110	2	S19672 Ig lambda chain V-
10	505.5	86.4	146	2	S02083 Ig lambda chain V-
11	502	85.8	96	2	S36060 Ig lambda chain -
12	502	85.8	115	2	S13726 Ig lambda chain V
13	494	84.4	233	2	S23741 Ig lambda chain -
14	430.5	73.6	106	2	S38495 Ig lambda chain -
15	408	69.7	105	2	S49533 anti-5m antibody V
16	407	69.6	119	2	S30526 Ig lambda chain V
17	407	69.6	120	2	S25740 Ig lambda chain -
18	385.5	65.9	120	2	S30525 Ig lambda chain V
19	385	65.8	107	2	PC4283 Ig lambda chain V
20	381	65.1	226	2	S25745 anti-SS-A/Ro 60K p
21	376	64.3	231	2	S25738 Ig lambda chain -
22	375.5	64.2	212	2	S70431 Ig lambda chain -
23	374	63.9	120	2	S30527 Ig lambda chain V
24	372	63.6	151	2	S25739 Ig lambda chain -
25	371	63.4	221	2	S25751 Ig lambda chain -
26	367	62.7	107	1	L4H0HL Ig lambda chain V-
27	366	62.6	231	2	S25753 Ig lambda chain -
28	364	62.2	109	2	S68171 Ig lambda chain V
29	362	61.9	111	2	S36274 Ig lambda chain V

30	362	61.9	233	2	S25747 Ig lambda chain -
31	358	61.2	108	1	L5H0DL Ig lambda chain V-
32	357	61.0	106	1	L4H0BU Ig lambda chain V-
33	355	60.7	132	2	S09713 Ig lambda chain V
34	351.5	60.1	112	2	S51148 antibody light cha
35	351.5	60.1	232	2	S25756 Ig lambda chain -
36	350	59.8	106	1	L4H0ML Ig lambda chain V-
37	348	59.5	106	1	L4H0X Ig lambda chain V-
38	346.5	59.2	236	2	S25746 Ig lambda chain -
39	346	59.1	105	2	S44124 Ig lambda chain V
40	344	58.8	130	1	L1H0BL Ig lambda chain pr
41	343	58.6	110	2	S57442 Ig lambda chain V-
42	342	58.5	95	2	S36065 Ig lambda chain -
43	342	58.5	114	2	S16440 Ig lambda chain -
44	341	58.3	128	2	S24319 Ig lambda chain pr
45	340	58.1	235	2	S05270 Ig lambda chain pr
46	339.5	58.0	112	2	S31515 Ig lambda chain V-
47	339	57.9	111	1	L2H0MC Ig lambda chain V-
48	339	57.9	111	2	S47009 Ig lambda chain V1
49	337.5	57.7	110	2	S51149 antibody light cha
50	336	57.4	129	2	S78058 Ig lambda chain pr
51	334	57.1	235	2	S14675 Ig lambda chain -
52	333.5	57.0	112	2	S44105 Ig lambda chain V-
53	333	56.9	106	1	L4H0XN Ig lambda chain V-
54	333	56.9	125	2	A31493 Ig light chain pre
55	333	56.9	216	2	S44193 Ig lambda chain (B
56	332.5	56.8	112	2	S44123 Ig lambda chain V-
57	330	56.4	111	1	L2H0BH Ig lambda chain V-
58	330	56.4	111	2	S47185 Ig lambda chain -
59	327	55.9	111	1	L1H0NG Ig lambda chain V-
60	326.5	55.8	217	2	JR0246 Ig lambda chain NI
61	326	55.7	130	2	S09712 Ig lambda chain V
62	325	55.6	111	1	L2H0VL Ig lambda chain V-
63	325	55.6	120	2	S30528 Ig lambda chain V
64	325	55.6	232	2	S25742 Ig lambda chain -
65	325	55.6	233	2	S25752 Ig lambda chain -
66	324	55.4	136	2	S16848 Ig lambda chain V-
67	324	55.4	213	2	JR0247 Ig lambda chain NI
68	323.5	55.3	112	1	L2H0NG Ig lambda chain V-
69	323	55.2	111	1	L6H0ST Ig lambda chain V-
70	322.5	55.1	213	2	S21066 Ig lambda chain V

## ALIGNMENTS

## RESULT 1

Ig lambda chain V region (clone alpha-BSA3) - human

C/Species: Homo sapiens (man)  
C/Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000  
C/Accession: S19663

R/Marks: J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter  
J. Mol. Biol. 222, 581-597, 1991

A/Title: By-passing immunization. Human antibodies displayed on pI  
A/Reference number: S19663; MUID:92085276; PMID:1748994

A/Accession: S19663

A/Molecule type: mRNA

A/Residues: 1-109 <MAR>  
A/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: heterodimer; immunoglobulin  
F/15-89/Domain: Immunoglobulin homology <IMM>

Query Match 95.0%; Score 556; DB 2; Length 109;  
Best Local Similarity 97.2%; Pred. No. 46-41;  
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SSELTPDPAVVALQGVTVVTCGDSLSYSYVYQKRGQAPVIVYIKNNRPSGIPDR 62  
DB 1 SSELTPDPAVVALQGVTVVTCGDSLSYSYVYQKRGQAPVIVYIKNNRPSGIPDR 60  
QY 63 FGGSSGNFASLTITGAQAEADYVCNSRDSGNHWVFGGTELTVLG 111

Db 61 FSSSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGKTIVLG 109

## RESULT 2

S38498  
Ig lambda chain - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C/Accession: S38498  
R/Marks: J.D.; Ouweland, W.H.; Bye, J.M.; Finmer, R.; Gorick, B.D.; Voak, D.; Thorpe, S.  
Submitted to the EMBL Data Library, June 1993  
A/Description: Human antibody fragments specific for human blood group antigens from a B-lymphocyte.  
A/Reference number: S38498  
A/Accession: S38498  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-108 <MAR>  
A/Cross-references: EMBL:Z23035; NID:G414043; PIDN:CAA80570.1; PID:G414044  
A/Superfamily: immunoglobulin V region; immunoglobulin homology  
A/Keywords: heterotetramer; immunoglobulin  
F/14-88/Domain: immunoglobulin homology <IMM>

Query Match 94.0%; Score 550; DB 2; Length 108;  
Best Local Similarity 96.3%; Pred. No. 1.3e-40;  
Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 SSELTPDAVSAVGQTVRTVTCQGDLSRSYASWYQKPGQAPLVITYGKNNRPSGIPDR 63  
Db 1 SSELTPDAVSAVGQTVRTVTCQGDLSRSYASWYQKPGQAPLVITYGKNNRPSGIPDR 60  
Qy 64 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGKTIVLG 111  
Db 61 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGKTIVLG 108

## RESULT 3

S47184  
Ig lambda chain - human  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C/Accession: S47184  
R/Marks: R.S.; Tandon, N.; Meccalfe, R.A.; Weetman, A.P.  
Submitted to the EMBL Data Library, June 1994  
A/Description: Cloning and analysis of Igm anti-thyroglobulin autoantibodies from patient  
A/Reference number: S47181  
A/Accession: S47184  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-108 <MC1>  
A/Cross-references: EMBL:X79783; NID:G506426; PIDN:CAA56179.1; PID:G506427  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-89/Domain: immunoglobulin homology <IMM>

Query Match 94.0%; Score 550; DB 2; Length 108;  
Best Local Similarity 97.2%; Pred. No. 1.3e-40;  
Matches 105; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SSELTPDAVSAVGQTVRTVTCQGDLSRSYASWYQKPGQAPLVITYGKNNRPSGIPDR 62  
Db 1 SSELTPDAVSAVGQTVRTVTCQGDLSRSYASWYQKPGQAPLVITYGKNNRPSGIPDR 60  
Qy 63 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGKTIVLG 110  
Db 61 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGKTIVLG 108

## RESULT 4

S70444  
Ig lambda chain precursor V region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 21-Jan-2000

C/Accession: S70444; S70426  
R/Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.  
Mol. Immunol. 29, 1363-1373, 1992

A/Title: Igm kappa/lambda EBV human B cell clone: an early step of differentiation of fe  
A/Reference number: S70444; PMID:93024508; PMID:1383695

A/Accession: S70444  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-127 <CU1>  
A/Experimental source: clone E29.1  
R/Tonnelle, C.

A/Reference number: S70426  
A/Accession: S70426

A/Molecule type: mRNA  
A/Residues: 1-90 <TON>  
A/Cross-references: EMBL:X53070  
A/Experimental source: cell line E29.1, clone VL 29-1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/1-20/Domain: signal sequence #status predicted <SIG>  
F/21-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>  
F/34-108/Domain: immunoglobulin homology <IMM>

Query Match 93.0%; Score 544; DB 2; Length 127;  
Best Local Similarity 95.4%; Pred. No. 5e-40;  
Matches 103; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SSELTPDAVSAVGQTVRTVTCQGDLSRSYASWYQKPGQAPLVITYGKNNRPSGIPDR 62  
Db 20 SSELTPDAVSAVGQTVRTVTCQGDLSRSYASWYQKPGQAPLVITYGKNNRPSGIPDR 79  
Qy 63 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGKTIVLG 110  
Db 80 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGKTIVLG 127

## RESULT 5

S36272  
Ig lambda chain V region (clone alpha-THY-29) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C/Accession: S36272  
R/Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
EMBO J. 12, 725-734, 1993  
A/Title: Human anti-self antibodies with high specificity from phage display libraries.  
A/Reference number: S36256; PMID:9317848; PMID:7679990  
A/Accession: S36272  
A/Status: preliminary; nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-110 <GRI>  
A/Cross-references: EMBL:Z18833; NID:G33419; PIDN:CAA79285.1; PID:G939912  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-89/Domain: immunoglobulin homology <IMM>

Query Match 92.2%; Score 539.5; DB 2; Length 110;  
Best Local Similarity 95.5%; Pred. No. 1.1e-39;  
Matches 105; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 3 SSELTPDAVSAVGQTVRTVTCQGDLSRSYASWYQKPGQAPLVITYGKNNRPSGIPDR 62  
Db 1 SSELTPDAVSAVGQTVRTVTCQGDLSRSYASWYQKPGQAPLVITYGKNNRPSGIPDR 60  
Qy 63 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGKTIVLG 111  
Db 61 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGKTIVLG 110

## RESULT 6

S38496  
Ig lambda chain - human (fragment)  
C/Species: Homo sapiens (man)



C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C/Accession: S38496  
R/Marks, J.D.: Ouweland, W.H.; Bye, J.M.; Rimmern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.  
submitted to the EMBL Data Library, June 1993  
A/Description: Human antibody fragments specific for human blood group antigens from a P  
A/Reference number: S38488  
A/Accession: S38496  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-109 <MAR>  
A/Cross-references: EMBL:Z23031; NID:G414039; PIDN:CAA80566.1; PID:G414040  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 90.1%; Score 527; DB 2; Length 109;  
Best Local Similarity 90.8%; Pred. No. 1.2e-38;  
Matches 99; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

3 SSELTDPAVSVALGQTVRTTCGDSLSRSYASWYQKPGQAPLVLYIGKNNRPSGIPDR 62  
1 SSELTDPAVSVALGQTVRTTCGDSLSRSYASWYQKPGQAPLVLYIGKNNRPSGIPDR 60  
63 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFSGGTETLVLG 111  
61 FSGSSSGNTASLTITGAQAEADADYYCTSRDTSGNHVLFGGKTLVLG 109

RESULT 7  
S25748  
Ig lambda chain - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C/Accession: S25748  
R/Comdrato, G.; Klobbeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A/Title: V(lambda) and J(lambda) gene segments of the human immunoglobulin lam  
A/Reference number: S16439; MUID:91257162; PMID:1904362  
A/Accession: S25748  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-233 <COM>  
A/Cross-references: EMBL:X57813; NID:G33725; PIDN:CAA0950.1; PID:G33726  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 88.5%; Score 518; DB 2; Length 233;  
Best Local Similarity 89.0%; Pred. No. 1.6e-37;  
Matches 97; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

3 SSELTDPAVSVALGQTVRTTCGDSLSRSYASWYQKPGQAPLVLYIGKNNRPSGIPDR 62  
20 SSELTDPAVSVALGQTVRTTCGDSLSRSYASWYQKPGQAPLVLYIGKNNRPSGIPDR 79  
63 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFSGGTETLVLG 111  
80 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFSGGTETLVLG 128

RESULT 8  
I3HUSH  
Ig lambda chain V-III region (Sh) - human  
C/Species: Homo sapiens (man)  
C/Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 02-Sep-1997  
C/Accession: A01980  
R/Titani, K.; Wikler, M.; Shinoda, T.; Putnam, F.W.  
J. Biol. Chem. 245, 2171-2176, 1970  
A/Title: The amino acid sequence of a lambda type Bence-Jones protein. III. The complete  
A/Reference number: A92057; MUID:70166723; PMID:4909564  
A/Accession: A01980  
A/Molecule type: protein  
A/Residues: 1-108 <TIT>

A/Note: the sequence of the C region is also given  
C/Genetics:  
A/Gene: GDB:IGLV8  
A/Cross-references: GDB:119342; OMIM:147240  
A/Map position: 22q11.2-22q11.2  
A/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka)  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1.  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:14-88/Domain: immunoglobulin homology <IMM>  
F:21-86/Disulfide bonds: #status experimental

Query Match 88.0%; Score 515; DB 1; Length 108;  
Best Local Similarity 89.8%; Pred. No. 1.3e-37;  
Matches 97; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

4 SELTDPAVSVALGQTVRTTCGDSLSRSYASWYQKPGQAPLVLYIGKNNRPSGIPDR 63  
1 SELTDPAVSVALGQTVRTTCGDSLSRSYASWYQKPGQAPLVLYIGKNNRPSGIPDR 60  
64 SGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFSGGTETLVLG 111  
61 SGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFSGGTETLVLG 108

RESULT 9  
S19672  
Ig lambda chain V region (clone alpha-TEL14) - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000  
C/Accession: S19672  
R/Marks, J.D.; Hoogenboom, H.R.; Bonnet, T.P.; McCafferty, J.; Griffiths, A.D.; Winter  
J. Mol. Biol. 222, 581-597, 1991  
A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on p  
A/Reference number: S19663; MUID:92085276; PMID:1748994  
A/Accession: S19672  
A/Molecule type: mRNA  
A/Residues: 1-110 <MAR>  
A/Cross-references: EMBL:X61644; NID:G37856; PIDN:CAA43825.1; PID:G1335384  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 87.3%; Score 510.5; DB 2; Length 110;  
Best Local Similarity 90.0%; Pred. No. 3.3e-37;  
Matches 99; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

3 SSELTDPAVSVALGQTVRTTCGDSLSRSYASWYQKPGQAPLVLYIGKNNRPSGIPDR 62  
1 SSELTDPAVSVALGQTVRTTCGDSLSRSYASWYQKPGQAPLVLYIGKNNRPSGIPDR 60  
63 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFSGGTETLVLG 111  
61 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFSGGTETLVLG 110

RESULT 10  
S02083  
Ig lambda chain V-IV region - human (tentative sequence) (fragments)  
N/Alternate names: amyloid-fibril protein GIL  
C/Species: Homo sapiens (man)  
C/Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 31-Mar-2000  
C/Accession: S02083  
R/Fyke, E.M.; Sletten, K.; Husby, G.; Cornwell III, G.G.  
Biochem. J. 256, 973-980, 1988  
A/Title: The primary structure of the variable region of an immunoglobulin IV light-cha  
A/Reference number: S02083; MUID:89134210; PMID:3146981  
A/Accession: S02083  
A/Molecule type: protein  
A/Residues: 1-70;71-72;73-75;76-131;132-146 <FYK>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match	86.4%;	Score 505.5;	DB 2;	Length 146;
Best Local Similarity	88.9%;	Pred. No. 1.2e-36;		
Matches	96;	Conservative	9;	Mismatches 2;
				Indels 1;
				Gaps 1

<b>OY</b>	SELFQDPAVSV <sup>AL</sup> AGQTIVRTVCQGDSLS <sup>SYA</sup> SWQOKPFGCAPVLVYIGKNNRSGGIPDR	6
	: :	
<b>Db</b>	1 SELFQDPAVSV <sup>AL</sup> AGQTIVRTICQGD <sup>S</sup> LNPFA <sup>SW</sup> QOKPFGCAPLTVIYGKNNRPSGGIPBRF	60
<b>OY</b>	SGSSSGNTASTLTITGAQAEDADYYCNSPRDSSGN-HMVFGGGTETLV	110
	: :	
<b>Db</b>	61 SGSSSGNTASTLTITGAQAEDADYYCNSRRN <sup>S</sup> SGNYHVIIFGGGIRKTLTV	108

RESULT 11  
S36060  
Ig Lambda chain - human (fragment)  
C-terminus, Homo sapiens (man)

Submitted to the EMBL Data Library, April 1993

A:Reference number: S36046

A:Accession: S36060

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-96 <ML>

A:Cross-references: EMBL:Z22202; NID:G312325; PIDN:CA80211.1; PID:G312326

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-89/Domain: immunoglobulin homology <IMM>

QY S S E L T I O P P A V S V A L G O V R V A T I C G S D S L R S Y A S W Y O O K P C Q A P V L Y I Y G N N P S G I P D R 6 2 2

QY S S E L T I O P P A V S V A L G O V R V A T I C G S D S L R S Y A S W Y O O K P C Q A P V L Y I Y G N N P S G I P D R 6 2 2

Db 1 S S E L T I O P P A V S V A L G O V R I T I C G S D S L R S Y A S W Y O O K P C Q A P V L Y I Y G N N P S G I P D R 6 0 6

QY F S G S S G N T A S L I T T G A O A E D E A D Y I C N S R D S G N H 9 8

Db 6 1 F S G S S G N T A S L I T T G A O A E D E A D Y I C N S R D S G N H 9 6

RESULT 12  
S13726

lambda chain V region - human  
 Species: Homo sapiens (man)  
 Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
 C.Accession: S13726  
 R.Fripiat, J.P.; Chuchana, P.; Bernard, F.; Bulwela, L.; Lefranc, G.; Lefranc, M.P.  
 Nucleic Acids Res. 19, 7134, 1990  
 A.Title: First genomic sequence of a human Ig variable lambda gene belonging to subgroup  
 A.Reference number: S13726; MUID:91088295; PMID:212477  
 A.Accession: S13726  
 A.Status: preliminary  
 A.Molecule type: DNA  
 A.Residues: 1-115 <FR>  
 A.Cross-references: EMBL:X56178; NID:g33404; PID:CAA3639.1; PID:g33405  
 C.Genetics:  
 A.Introns: 16/1  
 C.Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C.Keywords: heterotrimer; immunoglobulin  
 F:34-108/Domain: immunoglobulin homology <IM>

Query Match	85.8%	Score 502	DB 2:	Length 115
Best Local Similarity	99.0%	Pred. No. 18-36		
Matches	95	Conservative	1	Mismatches 0
				Indels 0
				Gaps 0
Qy	3	SESLTODPAVSVALGQTVAVTCQGSLSRYISWYQKRGKQAPVLYIKANNRPSGIPR	62	
Db	20	SESLTODPAVSVALGQTVAVTCQGSLSRYISWYQKRGKQAPVLYIKANNRPSGIPR	79	

```
QY      63 FSGSSSGNTASLTITGAQAEDADYYCNSRDSSGNH   98
          |||||
DB       80 FSGSSSGNTASLTITGAQAEDADYYCNSRDSSGNH   11
```

```

RESULT 13
S25741
IG lambda chain - human
CISpecies: Homo sapiens (man)
CDate: 22-Nov-1993 #sequence_revision 26-May-1995 #ext_change 21-Jan-2000
CAccession: S25741
RCombiRato: G.; Klobbeck, H.G.
Eur. J. Immunol.: 21, 1513-1522, 1991
A>Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A:Reference number: S16439; MUID:91257162; PMID:11904362
A:Accession: S25741
A:Status: Preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-233 <CMB>
A:Cross-references: EMBL:X57805; NID:G33707; PIDN:CAA40943.1; PID:G33708
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F148-216/Domain: immunoglobulin homology <LTM>

```

Query Match	84.4%;	Score 494;	DB 2;	Length 233;
Best Local Similarity	85.2%;	Pred. No. 1.8e-35;		
Matches 92;	Conservative 9;	Mismatches 7;	Indels 0;	Gaps 0

OY	3	SSELTTOPPAVSVALGCVRTTCGGDBLSRYVASYASWYOQKCGQAAPVLVIYCKNNRPSGI	PDR	62
	:	: :	:	:
Db	20	SSELTTOPPYSAVALGOTLRICKCGDTRISYASWYOQKCGQAATLLINGKDNRP	SGSI PDR	79
OY				
Db	80	FSSGSSENTASTLITTTGAQADEADYYCNSPDSGHNHVFVGSGTETLVL		110
	:	:	:	:
	80	FSSGSTSNTASTLITTTGADEADYYCNSHDSSAHHLVFGGGTKTLTVL		127

RESULT 14  
S38495  
Ig lambda chain - human (fragment)  
C.Species: Homo sapiens (man)  
C.Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C.Accession: S38495  
R.Marks, J.D.; Onehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S  
submitted to the EMBL Data Library, June 1993  
A.Description: Human antibody fragments specific for human blood group antigens from a P  
A.Reference number: S38488  
A.Accession: S38495  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-106 <EMBL>  
A.Cross-references: NRD:Z23029; PIDN:CAA80564.1; PID:g414038  
C.Superfamily: immunoglobulin v region; immunoglobulin homology  
C.Keywords: heterotetramer; immunoglobulin  
F:15-89/Domain: immunoglobulin homology <IMM>

[illegible]

RESULT 15  
S49533  
anti-Sm antibody VL chain (V Lambda 3b/J Lambda 2/3) - human

C:Species: Homo sapiens (man)  
 C:Date: 01-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 21-Jan-2000  
 C:Accession: S49533  
 R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.  
 submitted to the EMBL Data Library, October 1994  
 A:Description: Molecular characterization of natural human anti-Sm autoantibodies.  
 A:Reference number: S48797  
 A:Accession: S49533  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-105 <MAH>  
 A:Cross-references: EMBL:246346; NID:G560845; PIDN:CAA86465.1; PID:G1340169  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 F:11-85/Domain: immunoglobulin homology <IMM>

Query Match 69.7%; Score 408; DB 2; Length 105;  
 Best Local Similarity 73.3%; Pred. No. 2e-28;  
 Matches 77; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

7	TDDPAVSVALGQTVRVTCGDSLSRYVYASWYQKPGQAPVLYGKNNRPSGI	PDRPSSG	66
1	TOPPSVSPGQPARITCSGDALPKQYAYWYQKPGQAPVLYKDSERPSSI	PERPSSG	60
67	SSGNTASLITTTGAQAEDEADYYCNSRDSGSHWVFGGTELTIVIG	111	
61	SSGTTVLTITISGVQAEDEADYYCQADSSGTYVFGGTELTIVIG	105	

Search completed: September 9, 2004, 11:07:25  
 Job time : 13.3333 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 9, 2004, 10:58:34 ; Search time 8.0641 Seconds  
(without alignments)  
716.730 Million cell updates/sec

Title: US-09-880-748-2\_COPY\_139\_249

Perfect score: 585

Sequence: 1 AFSSSLTQPPAVSVALGQTV.....RDSGNHWVGCGTELTIVIG 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	515	88.0	108	1	LV3A_HUMAN
2	367	62.7	107	1	LV4C_HUMAN
3	365	62.4	111	1	LV3B_HUMAN
4	358	61.2	108	1	LV5A_HUMAN
5	357	61.0	106	1	LV4A_HUMAN
6	350	59.8	106	1	LV4E_HUMAN
7	348	59.5	106	1	LV4B_HUMAN
8	344	58.8	130	1	LV1G_HUMAN
9	339	57.9	111	1	LV2F_HUMAN
10	333	56.9	106	1	LV4D_HUMAN
11	330	56.4	111	1	LV2C_HUMAN
12	327	55.9	111	1	LV1D_HUMAN
13	325	55.6	111	1	LV2H_HUMAN
14	323.5	55.3	112	1	LV2K_HUMAN
15	323	55.2	111	1	LV6C_HUMAN
16	322	55.0	111	1	LV2G_HUMAN
17	319	54.5	111	1	LV7A_HUMAN
18	315	53.8	109	1	LV1F_HUMAN
19	310	53.0	111	1	LV1C_HUMAN
20	309.5	52.9	112	1	LV6A_HUMAN
21	308	52.6	109	1	LV2E_HUMAN
22	308	52.6	111	1	LV2I_HUMAN
23	306.5	52.4	131	1	LV6E_HUMAN
24	303	51.8	111	1	LV2A_HUMAN
25	300	51.3	109	1	LV1I_HUMAN
26	298.5	51.0	110	1	LV2J_HUMAN
27	297	50.8	111	1	LV6B_HUMAN
28	296	50.6	111	1	LV2B_HUMAN
29	293.5	50.2	112	1	LV6B_HUMAN
30	293	50.1	111	1	LV2D_HUMAN
31	292	49.9	113	1	LV1I_CHICK
32	289.5	49.5	112	1	LV1B_HUMAN
33	288.5	49.3	112	1	LV1H_HUMAN

## ALIGNMENTS

RESULT 1	LV3A_HUMAN	STANDARD;	PRT;	108 AA.
AC	P01714;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DB	Ig lambda chain V-II region SH.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE:70166723; PubMed:4909564;			
RA	Tilani K., Wikler M., Shinoda T., Putnam F.W.;			
RT	"The amino acid sequence of a lambda type Bence-Jones protein. 3. The			
RT	complete amino acid sequence and the location of the disulfide			
RT	bridges."			
RU	J. Biol. Chem. 245:2171-2176 (1970).			
CC	-I- MISCELLANEOUS: This is a Bence-Jones protein.			
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.			
DR	PIR; A01980; L3HUSH.			
DR	HSSP; P80748; ZLOI.			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	GO; GO:0003823; F:antigen binding; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig_V.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig_1.			
DR	SMART; SM00406; IGV; 1.			

34	280	47.9	111	1	LV1A_HUMAN	P01699	homo sapien
35	279.5	47.8	129	1	LV1B_MOUSE	P01774	mus musculus
36	274.5	46.9	110	1	LV13_RABIT	P01694	oryctolagus
37	267.5	45.7	129	1	LV1D_MOUSE	P01726	mus musculus
38	267.5	45.7	129	1	LV1E_MOUSE	P01727	mus musculus
39	265.5	45.4	110	1	LV1C_MOUSE	P01725	mus musculus
40	261	44.6	111	1	LV2I_HUMAN	P80422	homo sapien
41	261	44.6	117	1	LV2I_RABIT	P01691	oryctolagus
42	254	43.4	103	1	LV1E_HUMAN	P01703	homo sapien
43	251.5	43.0	136	1	LV5B_MOUSE	P01634	mus musculus
44	247.5	42.3	108	1	LV1W_HUMAN	P01605	homo sapien
45	245	41.9	110	1	LV3P_MOUSE	P01668	mus musculus
46	244.5	41.8	110	1	LV01_RABIT	P01636	oryctolagus
47	244	41.7	129	1	LV3O_HUMAN	P18136	homo sapien
48	243.5	41.6	111	1	LV3O_MOUSE	P01657	mus musculus
49	243	41.5	133	1	LV4B_HUMAN	P06313	homo sapien
50	242.5	41.5	109	1	LV14_RABIT	P01695	oryctolagus
51	241.5	41.3	108	1	LV07_RABIT	P01688	oryctolagus
52	241.5	41.3	131	1	LV3J_MOUSE	P01661	mus musculus
53	241	41.2	108	1	LV6K_MOUSE	P04945	mus musculus
54	239.5	40.9	108	1	LV1B_MOUSE	P01594	homo sapien
55	239.5	40.9	110	1	LV15_RABIT	P01656	oryctolagus
56	239.5	40.9	111	1	LV3L_MOUSE	P01664	mus musculus
57	239	40.9	109	1	LV3E_HUMAN	P01623	homo sapien
58	238.5	40.8	111	1	LV3E_MOUSE	P01657	mus musculus
59	238.5	40.8	111	1	LV3H_MOUSE	P01660	mus musculus
60	238.5	40.8	111	1	LV3O_MOUSE	P01659	mus musculus
61	238.5	40.8	129	1	LV2B_MOUSE	P01729	mus musculus
62	237.5	40.6	134	1	LV4C_HUMAN	P06314	homo sapien
63	236.5	40.4	108	1	LV1H_HUMAN	P01600	homo sapien
64	236.5	40.4	109	1	LV03_RABIT	P01684	oryctolagus
65	236	40.3	129	1	LV3L_HUMAN	P18135	homo sapien
66	235.5	40.3	111	1	LV3W_MOUSE	P01665	mus musculus
67	235.5	40.3	114	1	LV4A_HUMAN	P01625	homo sapien
68	234.5	40.1	108	1	LV08_RABIT	P01689	oryctolagus
69	234.5	40.1	115	1	LV02_RABIT	P01683	oryctolagus
70	234	40.0	107	1	LV6A_MOUSE	P01675	mus musculus

DR PROSITE: PSS0835; IG-LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 97 IG-LIKE.  
FT DISULFID 21 86  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11392 MW; E7E129586411A56 CRC64;

Query Match  
Best Local Similarity 89.8%; Score 515; DB 1; Length 108;  
Matches 97; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 4 SELTDDPAVSVALGQTVRTVTCQGDLSRSYASWYQKPGQAPLVLYIGKNNRPSGIPDRF 63  
DB 1 SELTDDPAVSVALGQTVRTVTCQGDLSRGDAAWYQKPGQAPLVLYIGKNNRPSGIPDRF 60  
QY 64 SSSSSGNRTSLITTTGAQAEDEADYCNPSRDSGNNHWFGGTYLTVLG 111  
DB 61 SSSSSGNRTSLITTTGAQAEDEADYCNPSRDSGKHVLFGGTYLTVLG 108

LT 2  
ID HUMAN  
AC LV4C HUMAN STANDARD; PRT; 107 AA.  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-IV region H11.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=78187276; PubMed=418804;  
RA Lopez de Castro J.A., Chiu Y.-Y.H., Poljak R.J.;  
RT "Amino acid sequence of the variable region of the light (lambda)  
chain from human myeloma cryoimmunoglobulin IgG H11.";  
RL Biochemistry 17:1718-1723(1978).  
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS APPARENTLY  
IDENTICAL WITH THAT OF HUMAN SH LAMBDA CHAIN EXCEPT IN HAVING  
155-ILE (H1L NUMBERING) INSTEAD OF VAL.  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01983; L4HHL.  
DR HSSP; P80748; 2LOI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; P:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_V.

DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG-LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 97 IG-LIKE.  
FT NON TER 107 107  
SQ SEQUENCE 107 AA; 11517 MW; A5C8AFPE0CCG590A CRC64;

Query Match  
Best Local Similarity 62.7%; Score 367; DB 1; Length 107;  
Matches 70; Conservative 16; Mismatches 21; Indels 2; Gaps 1;

QY 3 SEELTDPAVSVALGQTVRTVTCQGDLSRSYASWYQKPGQAPLVLYIGKNNRPSGIPDR 62  
DB 1 SEELTDPAVSVALGQTVRTVTCQGDLSRSYASWYQKPGQAPLVLYIGKNNRPSGIPDR 60  
QY 63 FGGSSGNRTSLITTTGAQAEDEADYCNPSRDSGNNHWFGGTYLTVLG 111  
DB 61 FGGSSGNRTSLITTTGAQAEDEADYCNPSRDSGNNHWFGGTYLTVLG 107

RESULT 3

LV3B HUMAN  
ID LV3B HUMAN STANDARD; PRT; 111 AA.  
AC P80748;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-III region LOI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE, SUBUNIT, DISEASE, AND 3D-STRUCTURE MODELLING.  
RX TISSUE=Urine;  
RX MEDLINE=99441384; PubMed=10510403;  
RA Jokiranta T.S., Solomon A., Pangburn M.K., Zipfel P.F., Meri S.;  
RT "Nephritogenic lambda light chain dimer: a unique human  
miniautoantibody against complement factor H.";  
RL J. Immunol. 163:4590-4596(1999).

CC -1- FUNCTION: ACTIVATES THE ALTERNATIVE COMPLEMENT PATHWAY BY BINDING  
TO THE SHORT CONSENSUS REPEAT DOMAIN 3 (SCR3) OF FACTOR H.  
CC -1- SUBUNIT: Homodimer.  
CC -1- DISEASE: The blocking of factor H by LOI protein leads to the  
developmental of membranoproliferative glomerulonephritis (MPGN).  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PDB; 2LOI; 29-DEC-99.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; P:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG-LIKE; 1.  
KW Immunoglobulin V region; 3D-structure.  
FT DOMAIN 1 97 IG-LIKE.  
FT BINDING 15 15 SCR3.  
FT BINDING 25 25 SCR3.  
FT BINDING 29 29 SCR3.  
FT BINDING 48 51 SCR3.  
FT BINDING 94 94 SCR3.  
FT DISULFID 21 86 BY SIMILARITY.  
FT STRAND 4 4  
FT STRAND 8 8  
FT TURN 13 14  
FT STRAND 16 14  
FT STRAND 32 37  
FT TURN 38 40  
FT STRAND 41 46  
FT TURN 49 50  
FT STRAND 54 54  
FT TURN 55 55  
FT TURN 58 59  
FT STRAND 60 61  
FT STRAND 64 65  
FT TURN 66 67  
FT STRAND 68 74  
FT TURN 78 79  
FT STRAND 82 88  
FT TURN 91 93  
FT STRAND 97 98  
FT STRAND 102 104  
FT TURN 107 108  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 11935 MW; 69498BEFDE82053 CRC64;

Query Match  
Best Local Similarity 67.6%; Score 365; DB 1; Length 111;  
Matches 71; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 6 LTDDPAVSVALGQTVRTVTCQGDLSRSYASWYQKPGQAPLVLYIGKNNRPSGIPDRFG 65  
DB 3 LTDDPAVSVALGQTVRTVTCQGDLSRSYASWYQKPGQAPLVLYIGKNNRPSGIPDRFG 62







RT "A new lambda-chain gene."  
 RL Immunochimistry 12:643-652(1975).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RA Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,  
 RA Pangiotopoulos N.;  
 RT "Rotational allomerism and divergent evolution of domains in  
 RT immunoglobulin light chains."  
 RL Biochemistry 14:3953-3961(1975).  
 RN (4)  
 RP X-RAY CRYSTALLOGRAPHY.  
 RA MEDLINE=90133913; PubMed=2515285;  
 RA Ely K.R., Herron J.N., Harker M., Edmundson A.B.;  
 RT "three-dimensional structure of a light chain dimer crystallized in  
 RT water. Conformational flexibility of a molecule in two crystal  
 RT forms."  
 RL J. Mol. Biol. 210:601-615(1989).  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 CC -1- MISCELLANEOUS: THE MCG-TYPE C REGION APPEARS TO BE CORRELATED WITH  
 CC A VERY UNUSUAL V-REGION SUBSTITUTION, 103-THR ABOVE FOR GLY,  
 CC SUGGESTING THAT THE V-C JOINING MECHANISM IS NOT ALWAYS RANDOM.  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+  
 CC MARKERS.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A90381; L2HMC.  
 DR PDB; 2MCG; 15-JUL-92.  
 DR PDB; 1ABQ; 17-JUN-98.  
 DR PDB; 1DCL; 15-MAY-97.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; P:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PFO0047; Ig\_V.  
 DR SMART; SM00406; IGV\_1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure;  
 KW Pyroglutamate carboxylic acid.  
 FT DOMAIN 1 108  
 FT MOD\_RES 1 1  
 FT DISULFID 22 90  
 FT STRAND 5 5  
 FT STRAND 10 12  
 FT STRAND 18 23  
 FT STRAND 26 32  
 FT STRAND 36 40  
 FT TURN 42 43  
 FT TURN 50 51  
 FT STRAND 52 54  
 FT TURN 55 54  
 FT TURN 55 55  
 FT TURN 62 63  
 FT STRAND 66 68  
 FT STRAND 72 77  
 FT STRAND 82 84  
 FT HELIX 86 93  
 FT STRAND 99 101  
 FT STRAND 105 109  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 11558 MW; 7CC1D6E2FA3377BA CRC64;  
 Query Match 57.9%; Score 339; DB 1; Length 111;  
 Best Local Similarity 61.3%; Pred. No. 5.6e-27;  
 Matches 68; Conservative 17; Mismatches 22; Indels 4; Gaps 3;  
 QY 4 SETTOPAVSVALGQTVRVTCGSDS--LRSY-YASWYQKPGQAPVLYVYKNNRPSGIP 60  
 DB 2 SATLTPSPASGSLGSGSTISCTGSSDVGYNVSWYQAKAPKVIIVKRRSGVP 61  
 QY 61 DRFGSSSGNTASLTITGAQAEDEADYVYCNRRDSSGHNWFGGTELTVLG 111  
 DB 62 DRFGSGKSGNTASLTITGAQAEDEADYVYCNRRDSSGHNWFGGTELTVLG 111

RESULT 10  
 ID LV4D HUMAN STANDARD; PRT; 106 AA.  
 AC P01718;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig lambda chain V-IV region Kern.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN (1)  
 RP SEQUENCE.  
 RX MEDLINE=71150336; PubMed=5549568;  
 RA Fongeling H., Hese M., Hilschmann N.;  
 RT "Structural rule of antibodies. Primary structure of a monoclonal  
 RT immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-  
 RT protein Kern). V. The complete amino acid sequence and its genetic  
 RT interpretation."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ MARKER.  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A01984; LAHUKN.  
 DR HSSP; P80748; 21OI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; P:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PFO0047; Ig\_V.  
 DR SMART; SM00406; IGV\_1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 KW DOMAIN 1 102  
 FT DISULFID 21 86  
 FT NON\_TER 106 106  
 SQ SEQUENCE 106 AA; 11277 MW; C6B4A05B9CB43CBE CRC64;  
 Query Match 56.9%; Score 333; DB 1; Length 106;  
 Best Local Similarity 61.0%; Pred. No. 2.1e-26;  
 Matches 64; Conservative 19; Mismatches 20; Indels 2; Gaps 1;  
 QY 6 LTPDPAVSVALGQTVRVTCGSDSLASYSYASWYQKPGQAPVLYVYKNNRPSGIPDRFG 65  
 DB 3 LTPDPSVSVPQGTAVITCSGDLKTFVSWYQKPGQAPVLYVYHTSRPSEIPDRFG 62  
 QY 66 SSSGNTASLTITGAQAEDEADYVYCNRRDSSGHNWFGGTELTVL 110  
 DB 63 SSSGATATLTITGAQSVDEADYFCQTDYITTA--IFGGSTKLTVL 105  
 RESULT 11  
 ID LV2C HUMAN STANDARD; PRT; 111 AA.  
 AC P01706;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig lambda chain V-II region BOH.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN (1)  
 RP SEQUENCE.  
 RX MEDLINE=75115478; PubMed=804002;  
 RA Kohler H., Rudofsky S., Klusken L.;  
 RT "The primary structure of a human lambda II chain."  
 RL J. Immunol. 114:415-421(1975).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE OZ+ MARKER.  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

CC	-1	SIMILARITY: Contains 1 immunoglobulin-like domain.
DR	PIR: A01965	L1HNG.
DR	HSSP: P01703	7FAB.
DR	GO: GO:0005576	C:extracellular; NAS.
DR	GO: GO:0003823	E:antigen binding; NAS.
DR	GO: GO:0006955	P:immune response; NAS.
DR	InterPro: IPR007110	IG-like.
DR	InterPro: IPR003586	IG_v.
DR	Pfam: PF00047	IG_1.
DR	SMART: SM00405	IGV_1.
DR	PROSITE: PS00835	IG_LIKE_1.
KW	Immunoglobulin V region	Pyroglutamate carboxylic acid.
FT	DOMAIN	1 105
FT	MOD_RES	1 1
FT	DISULFID	22 89
FT	NON_TER	111 111
SQ	SEQUENCE	111 AA; 11454 MW; A21C6121C18A61E0 CRC64;
Query Match	55.9%	Score 327; DB 1; Length 111;
Best Local Similarity	60.0%	Pred. No. 8, 7e-26;
Matches 66; Conservative 12; Mismatches 30; Indels 2; Gaps 1		

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Query Match          55.64; Score 325; DB 1; Length 111;
Best Local Similarity 62.28; Pred. No. 1.4e-25;
Matches 69; Conservative 13; Mismatches 25; Indels 4; Gaps

OY      4 SELTQDAVSVALGQTVRYTCGDS--LRSY-YASWYQKPKGAPVLVYGNKNRPSGIP 60
      |||:::||||:::||||:::||||:::||||:::||||:::||||:::
Db      2 SALIQPASVSGSGIGQSTITISCTGSSDVGGYVSWFQGHPTAPLITSEVNRPSGS 61
      |||:::||||:::||||:::||||:::||||:::||||:::||||:::
OY      61 DREGSSSGNTASLTITGAQADEADAYYCNRSRSGNMHWFGGTELTUG 111
      |||:::||||:::||||:::||||:::||||:::||||:::||||:::
Db      62 DRFGSGKSANTASLTISGLQADEADAYYCSSYTS--NSVFGGXTLYVG 111
      |||:::||||:::||||:::||||:::||||:::||||:::||||:::

RESULT 14
LV2K_HUMAN
ID      LV2K_HUMAN          STANDARD;          PRT;          112 AA.
AC      P04209;
DT      20-MAR-1987 (Rel. 04, Created)
DT      20-MAR-1987 (Rel. 04, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Iq lambda chain V-II region NIG-84.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI    OX      NCBT_TaxID=9606;
RN      [1]

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 9, 2004, 11:01:20 ; Search time 34.1538 Seconds  
(without alignments)  
1025.434 Million cell updates/sec

Title: US-09-880-748-2\_COPY\_139\_249

Perfect score: 585

Sequence: 1 AFSSSLTQPAVSVALGQTV.....ROSSGNHWVFGGTELTIVIG 111

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 70 summaries

Database :

SPTRMBL\_25:\*

1: sp\_bacteria:\*

2: sp\_fungi:\*

3: sp\_human:\*

4: sp\_invertebrate:\*

5: sp\_mammal:\*

6: sp\_mhc:\*

7: sp\_organellar:\*

8: sp\_phage:\*

9: sp\_plant:\*

10: sp\_rodent:\*

11: sp\_virus:\*

12: sp\_vertebrate:\*

13: sp\_unclassified:\*

14: sp\_viruses:\*

15: sp\_bacteriap:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	544	93.0	107	4	Q9NSD6
2	438	74.9	233	4	Q8TBC9
3	427	73.0	233	4	Q8NSF4
4	419	71.6	81	4	Q7Z2E8
5	367.5	62.8	234	4	Q8N355
6	366.5	62.6	107	4	Q9UL82
7	346	59.1	237	4	Q8WUK4
8	340	58.1	237	4	Q8WUK6
9	335.5	57.4	236	4	Q96E61
10	332.5	56.8	234	4	Q7Z2U7
11	323	55.2	116	4	Q96JDU
12	322.5	55.1	112	4	Q96JDI
13	319	54.5	110	4	Q8TE63
14	316	54.0	112	4	Q96JDU
15	308.5	52.7	236	4	Q8NEJ1
16	301	51.5	233	4	Q96JDU

## ALIGNMENTS

RESULT 1

Q9NSD6

Q9NSD6; PRELIMINARY; PRT; 107 AA.

01-OCT-2000 (TREMBLrel. 15, Created)

01-OCT-2003 (TREMBLrel. 15, Last sequence update)

01-OCT-2003 (TREMBLrel. 25, Last annotation update)

Hypothetical protein (Fragment).

Hom sapiens (Human).

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_Taxid=9606;

MBI [1]

SEQUENCE FROM N.A.

17	297	50.8	101	4	Q81ZD8	Q81ZD8 homo sapien
18	275	47.0	108	4	Q96SBO	Q96SBO homo sapien
19	270	46.2	235	11	Q99M11	Q99M11 mus musculu
20	267.5	45.7	129	11	Q8VDE2	Q8VDE2 mus musculu
21	267	45.6	113	11	Q8CGS1	Q8CGS1 mus musculu
22	255.5	43.7	131	11	Q81IC3	Q81IC3 mus musculu
23	248.5	42.5	108	4	Q9UL77	Q9UL77 homo sapien
24	248	42.4	134	11	Q8VDD0	Q8VDD0 mus musculu
25	247.5	42.3	240	4	Q8WUK3	Q8WUK3 homo sapien
26	245	41.9	107	4	Q9UL81	Q9UL81 homo sapien
27	245	41.9	109	11	Q9ET13	Q9ET13 mus musculu
28	244	41.7	109	4	Q9UL78	Q9UL78 homo sapien
29	244	41.7	235	11	Q7TMK0	Q7TMK0 mus musculu
30	243	41.5	107	4	Q96SAG	Q96SAG homo sapien
31	237	40.5	114	11	Q8K1F1	Q8K1F1 mus musculu
32	235	40.2	112	11	Q8K1F2	Q8K1F2 mus musculu
33	233.5	39.9	109	11	Q9Z0E6	Q9Z0E6 mus musculu
34	233	39.8	109	4	Q9UL85	Q9UL85 homo sapien
35	232	39.7	112	11	Q8K1F3	Q8K1F3 mus musculu
36	230	39.3	239	4	Q8TCD0	Q8TCD0 homo sapien
37	229.5	39.2	108	4	Q9UL70	Q9UL70 homo sapien
38	229.5	39.2	298	11	Q9QYF0	Q9QYF0 mus musculu
39	229	39.1	101	11	Q9JL78	Q9JL78 mus musculu
40	228.5	39.1	111	11	Q81IU6	Q81IU6 mus musculu
41	228	39.0	109	4	Q9UL86	Q9UL86 homo sapien
42	228	39.0	112	11	Q8K1F0	Q8K1F0 mus musculu
43	227.5	38.9	111	11	Q9Z0E9	Q9Z0E9 mus musculu
44	226.5	38.7	234	11	Q8VCP0	Q8VCP0 mus musculu
45	226.5	38.7	237	13	Q7S236	Q7S236 xenopus lae
46	226	38.6	106	5	Q9U410	Q9U410 schistosoma
47	224.5	38.4	107	11	Q9ERZ9	Q9ERZ9 mus musculu
48	224.5	38.4	109	6	Q9N0W5	Q9N0W5 oryctolagus
49	224.5	38.4	234	4	Q7Z473	Q7Z473 homo sapien
50	223	38.1	97	11	Q9JL76	Q9JL76 mus musculu
51	223	38.1	103	11	Q9JL80	Q9JL80 mus musculu
52	222.5	38.0	108	4	Q9UL83	Q9UL83 homo sapien
53	222.5	38.0	236	4	Q7Z3Y4	Q7Z3Y4 mus musculu
54	221	37.8	99	11	Q9JL74	Q9JL74 mus musculu
55	220	37.6	243	11	Q7TQW2	Q7TQW2 mus musculu
56	219.5	37.5	114	4	Q9UL80	Q9UL80 homo sapien
57	219.5	37.5	236	11	Q7TS98	Q7TS98 mus musculu
58	219	37.4	238	11	Q99M37	Q99M37 mus musculu
59	217.5	37.2	214	11	Q9RIAS	Q9RIAS mus musculu
60	217	37.1	239	11	Q8VCS5	Q8VCS5 mus musculu
61	216.5	37.0	230	4	Q7Z2U3	Q7Z2U3 homo sapien
62	214.5	36.7	108	4	Q9UL79	Q9UL79 homo sapien
63	214.5	36.7	108	11	Q8VTD0	Q8VTD0 mus musculu
64	214	36.6	238	11	Q8VC16	Q8VC16 mus musculu
65	213.5	36.5	236	11	Q7TMK3	Q7TMK3 mus musculu
66	211.5	36.2	233	11	Q91W59	Q91W59 mus musculu
67	210	35.9	235	11	Q91W12	Q91W12 mus musculu
68	206.5	35.3	104	11	Q9JL82	Q9JL82 mus musculu
69	200	34.2	248	13	Q7SYU1	Q7SYU1 xenopus lae
70	199	34.0	241	11	Q921A6	Q921A6 mus musculu

```
RC TISSUE=Lymphocytes;
RA "Autism A.;"
RL "Autism A.;"
DR EMBL; 143092; AAA69746.2; -.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match
Best Local Similarity 93.0%; Score 544; DB 4; Length 107;
Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 ELTQDPVAVSVALGQTVRVTCQGDLSRSYASWYQKRGQAPVLYVYIGKNNRPSGIPDR 64
1 ELTQDPVAVSVALGQTVRVTCQGDLSRSYASWYQKRGQAPVLYVYIGKNNRPSGIPDR 60
DB 65 GSSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGTELTVLG 111
61 GSSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGTELTVLG 107

RESULT 2
OY 08TBC9 PRELIMINARY; PRT; 233 AA.
AC 08TBC9;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022823; AAH22823.1; -.
DR PIR; S12442; S12442.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24867 MW; 367411BFDE4DF92 CRC64;

Query Match
Best Local Similarity 74.9%; Score 438; DB 4; Length 233;
Matches 82; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

OY 3 SSELTPDPAVSVALGQTVRVTCQGDLSRSYASWYQKRGQAPVLYVYIGKNNRPSGIPDR 62
20 SYELTPSPVSVPQGTARITCSGDALPKQYAVWYQKRGQAPVLYVYIGKNNRPSGIPDR 79
OY 63 FEGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGTELTVLG 111
80 FEGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGTELTVLG 128

RESULT 3
OY 08NSP4
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ID 08NSP4 PRELIMINARY; PRT; 233 AA.
AC 08NSP4;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hodgkin lymphoma, and Mantle cell lymphoma;
RA Tinguely M., Rosenquist R., Sundstroem C., Amiri R.M., Kupperts R.,
RA Hansmann M.L., Branninger A.;
RT "Analysis of a clonally related mantle cell and Hodgkin lymphoma
RT indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg
RT cell precursor in a germinal center."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ564423; CAD92030.1; -.
DR EMBL; AJ564424; CAD92031.1; -.
FT NON_TER 1
FT NON_TER 81
FT NON_TER 81
SQ SEQUENCE 81 AA; 8702 MW; CFF1D466B794C9F CRC64;

OY 3 SSELTPDPAVSVALGQTVRVTCQGDLSRSYASWYQKRGQAPVLYVYIGKNNRPSGIPDR 62
20 SYELTPSPVSVPQGTARITCSGDALPKQYAVWYQKRGQAPVLYVYIGKNNRPSGIPDR 79
OY 63 FEGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGTELTVLG 111
80 FEGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHWVFGGTELTVLG 128

RESULT 4
OY 07Z2E8 PRELIMINARY; PRT; 81 AA.
AC 07Z2E8;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Rearranged V131 segment (Rearranged V131 gene segment)
DE (Fragment).
GN V13L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hodgkin lymphoma, and Mantle cell lymphoma;
RA Tinguely M., Rosenquist R., Sundstroem C., Amiri R.M., Kupperts R.,
RA Hansmann M.L., Branninger A.;
RT "Analysis of a clonally related mantle cell and Hodgkin lymphoma
RT indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg
RT cell precursor in a germinal center."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ564423; CAD92030.1; -.
DR EMBL; AJ564424; CAD92031.1; -.
FT NON_TER 1
FT NON_TER 81
FT NON_TER 81
SQ SEQUENCE 81 AA; 8702 MW; CFF1D466B794C9F CRC64;
```

Query Match 71.6%; Score 419; DB 4; Length 81;  
Best Local Similarity 95.1%; Pred. No. 5.5e-35;  
Matches 77; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 22 VTGQDLSRSYASWTQKFGQAPVLVYIGKNNRPSGIPRFGSSSGNTASLTITGAQA 81  
1 ITCQGSLSFSYASWTQKFGQAPVLVYIGKNNRPSGIPRFGSSSGNTASLTITGAQA 60

DB 82 EDEADYYCNSRDSSGNHMFVG 102  
61 EDEADYYCNSRDSSGNHMFVG 81

## RESULT 5

ID Q8N355 PRELIMINARY; PRT; 234 AA.  
AC Q8N355;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
Hypothetical protein.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Strausberg R.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC028090; AAH28090.1; -

DR PIR; S12441; S12441.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG\_c1.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_V.

DR Pfam; PF00047; IG\_2.

DR SMART; SM00409; IG\_2.

DR SMART; SM00407; IGc1.1.

DR SMART; SM00406; IGc1.1.

DR PROSITE; PS00835; IG\_LIKE; 2.

DR PROSITE; PS00290; IG\_MHC; 1.

KW Hypothetical protein.

SO SEQUENCE 234 AA; 24792 MW; CC848CAEBA4A9D63 CRC64;

Query Match

62.8%; Score 367.5; DB 4; Length 234;  
Best Local Similarity 67.3%; Pred. No. 3.4e-29;

Matches 72; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

QY 6 LTQDPVAVSLGQTVAVTCQGSLSRSYASWTQKFGQAPVLVYIGKNNRPSGIPRFG 65  
23 LTQDPVAVSLGQTVAVTCQGSLSRSYASWTQKFGQAPVLVYIGKNNRPSGIPRFG 82

QY 66 SSSGNTASLTITGAQAEDADYYCNSRDSSGNH-MYFGGTELTVLG 111  
83 SSSGNTASLTITGAQAEDADYYCNSRDSSGNH-MYFGGTELTVLG 129

## RESULT 6

ID Q9UL82 PRELIMINARY; PRT; 107 AA.

AC Q9UL82;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
Myosin-reactive immunoglobulin light chain variable region  
(Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxId=9606;  
RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berny S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035032; AAD56268.1; -

DR HSP; P01703; 7FAB.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG\_V.

DR Pfam; PF00047; IG\_1.

DR SMART; SM00406; IGc1.1.

DR PROSITE; PS00835; IG\_LIKE; 1.

FT NON\_TER 1 -1

FT NON\_TER 107 107

SO SEQUENCE 107 AA; 11445 MW; 52FOC1AB36821DC CRC64;

Query Match 62.6%; Score 366.5; DB 4; Length 107;  
Best Local Similarity 67.6%; Pred. No. 1.6e-29;

Matches 73; Conservative 10; Mismatches 24; Indels 1; Gaps 1;

QY 3 SSELTPDPAVSLGQTVAVTCQGSLSRSYASWTQKFGQAPVLVYIGKNNRPSGIPR 62  
1 SYELTPDPAVSLGQTVAVTCQGSLSRSYASWTQKFGQAPVLVYIGKNNRPSGIPR 60

QY 63 FSGSSSGNTASLTITGAQAEDADYYCNSRDSSGNHMYFGGTELTVL 110  
61 FSGSSSGNTASLTITGAQAEDADYYCNSRDSSGNHMYFGGTELTVL 107

## RESULT 7

ID Q8WUK4 PRELIMINARY; PRT; 237 AA.

AC Q8WUK4;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxId=9606;  
RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Tomail;

RA Strausberg R.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC020233; AAH20233.1; -

DR PIR; S12441; S12441.

DR PIR; S12627; S12627.

DR PIR; S29258; S29258.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_V.

DR Pfam; PF00047; IG\_2.

DR SMART; SM00406; IGc1.1.

DR PROSITE; PS00835; IG\_LIKE; 2.

DR PROSITE; PS00290; IG\_MHC; 1.

KW Hypothetical protein.

SO SEQUENCE 237 AA; 24897 MW; 73C7D70B8039D186 CRC64;

Query Match 59.1%; Score 346; DB 4; Length 237;  
Best Local Similarity 64.3%; Pred. No. 5.1e-27;

Matches 72; Conservative 8; Mismatches 28; Indels 4; Gaps 2;

QY 4 SELTPDPAVSLGQTVAVTCQGSLSRSYASWTQKFGQAPVLVYIGKNNRPSGIP 60  
21 SELTPDPAVSLGQTVAVTCQGSLSRSYASWTQKFGQAPVLVYIGKNNRPSGIP 80

QY 61 DRFGSSSGNTASLTITGAQAEDADYYCNSRDSS-GNHMYFGGTELTVLG 111  
81 DRFGSSSGNTASLTITGAQAEDADYYCNSRDSS-GNHMYFGGTELTVLG 132





DT 01-DEC-2001 (T-EMBLrel. 19, Created)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
DE Amyloid lambda 6 light chain variable region SAR (Fragment).  
OS Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=bone marrow;  
RA Perfecti V., Casarini S., Colli Vignarelli M., Merlini G.;  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF267875; AAKS8587.1; -  
DR InterPro; IPR007110; IG\_1like.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IG\_1.  
DR PROSITE; PSS0835; IG\_1like; 1.  
FT NON\_TER 1  
SQ SEQUENCE 116 AA; 12294 MW; F7B0E9F49FAE369E CRC64;  
Query Match 55.1%; Score 323; DB 4; Length 116;  
Best Local Similarity 59.1%; Pred. No. 4.5e-25;  
Matches 65; Conservative 15; Mismatches 26; Indels 4; Gaps 2;  
QY 6 LTQDPVAVSALGQTVRTCCGD--SLRSYASVYQKPGQAPVLYIGKNNRPSGIPDRF 63  
DB 4 LTQPHVSSEPKGTIVTISCSSGSIATNVQYQARPSGAPFTVIYEDNRSGVPRDF 63  
QY 64 SGS--SSGNTASTLTGAQAEADYCCNSRDSGNNHWFGGTELTVLG 111  
DB 64 SSGIDSSNSASLTISGLKTEDEADYCCQSYDSSIGNVIFGGGKTLVLG 113  
RESULT 12  
ID 096J01 PRELIMINARY; PRT; 112 AA.  
AC 096J01;  
DT 01-DEC-2001 (T-EMBLrel. 19, Created)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
DE Amyloid lambda 6 light chain variable region PIP (Fragment).  
OS Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=bone marrow;  
RA Perfecti V., Casarini S., Colli Vignarelli M., Merlini G.;  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF267874; AAKS8586.1; -  
DR PIR; A30323; A30323.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IG\_1.  
DR PROSITE; PSS0835; IG\_1like; 1.  
FT NON\_TER 1  
SQ SEQUENCE 112 AA; 12047 MW; 0D3885AC23567B9F CRC64;  
Query Match 55.1%; Score 322.5; DB 4; Length 112;  
Best Local Similarity 59.1%; Pred. No. 4.9e-25;  
Matches 65; Conservative 16; Mismatches 24; Indels 5; Gaps 3;  
QY 6 LTQDPVAVSALGQTVRTCC--QGDLSLSYASVYQKPGQAPVLYIGKNNRPSGIPDRF 63  
DB 4 LTQPHVSSEPKGTIVTISCSSGSIATNVQYQARPSGAPFTVIYEDNRSGVPRDF 63

QY 64 SGS--SSGNTASTLTGAQAEADYCCNSRDSGNNHWFGGTELTVLG 111  
DB 64 SSGIDSSNSASLTISGLKTEDEADYCCQSYDSSIGNVIFGGGKTLVLG 112  
RESULT 13  
ID 08TE63 PRELIMINARY; PRT; 110 AA.  
AC 08TE63;  
DT 01-JUN-2002 (T-EMBLrel. 21, Created)  
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
DE Immunoglobulin light chain variable region (Fragment).  
OS Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95007525; PubMed=7923137;  
RA Hall B.U., Murray J.H., Haspel M.V., Kobrin B.J.;  
RT "Establishment, molecular rescue, and expression of 123AVL6-1, a  
RT tumor-reactive human monoclonal antibody.";  
RL Cancer Res. 54:5178-5185(1994).  
DR EMBL; L33985; AAL68704.1; -  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IG\_1.  
DR PROSITE; PSS0835; IG\_1like; 1.  
FT NON\_TER 1  
SQ SEQUENCE 110 AA; 11479 MW; 599D1628F8F5437C CRC64;  
Query Match 54.5%; Score 319; DB 4; Length 110;  
Best Local Similarity 58.7%; Pred. No. 1.1e-24;  
Matches 64; Conservative 13; Mismatches 30; Indels 2; Gaps 1;  
QY 4 SELLTDPVAVSALGQTVRTCCGDS--LSRSYASVYQKPGQAPVLYIGKNNRPSGIPDRF 61  
DB 2 SALTQPPSVSAAFGQVTVTISCSSGSIATNVQYQARPSGAPFTVIYEDNRSGVPRDF 61  
QY 62 RFSGSSGNTASTLTGAQAEADYCCNSRDSGNNHWFGGTELTVL 110  
DB 62 RFSGSSGNTASTLTGAQAEADYCCNSRDSGNNHWFGGTELTVL 110  
RESULT 14  
ID 096J02 PRELIMINARY; PRT; 112 AA.  
AC 096J02;  
DT 01-DEC-2001 (T-EMBLrel. 19, Created)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
DE Amyloid lambda 6 light chain variable region NEG (Fragment).  
OS Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=bone marrow;  
RA Perfecti V., Casarini S., Colli Vignarelli M., Merlini G.;  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF267873; AAKS8585.1; -  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IG\_1.  
DR PROSITE; PSS0835; IG\_1like; 1.  
FT NON\_TER 1

